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## SEARCH REQUEST FORM

Scie	ntific and Tech	nical Information Center	
Pequecier's Fill Name:		Examiner # :	Date:
Requester's Full Name: Phone Nu	ımber 30	Serial Number:	PINE PIOU FACE
Art Unit: Phone No.  Mail Box and Bldg/Room Location:		Results Format Preferred (circ	le): PAPER DISK E-MAIL
more than one search is submit			
lease provide a detailed statement of the so- nelude the elected species or structures, ke tility of the invention. Define any terms the nown. Please attach a copy of the cover sh	earch topic, and des ywords, synonyms, hat may have a spec	eribe as specifically as possible the acronyms, and registry numbers, are all meaning. Give examples or rele	subject matter to be searched.  Id combine with the concept or
Fitle of Invention:		•	
(nventors (please provide full names): _			
Earliest Priority Filing Date:			
*For Sequence Searches Only* Please includes appropriate serial number.	de all pertinent inforn	nation (parent, child, divisional, or issu	ued patent numbers) along with the
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STAFF USE ONLY	Type of Sear	<b>C.</b>	l cost where applicable
Searcher: Beverly C. 499	NA Sequence (#		
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Date Searcher Picked Up	Bibliographic	Lexis/Nexis	
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Searcher Prep & Review Time		WWW/Internet	
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PTO-1590 (1-2000)



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Minimum DB
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Rickettsia surface la		, Dobson ME;			•				layer; vaccine; typhus ease.	in.			1612 AA.	ALIGNMENTS	AAW86371 AAW86366 AAW86369 AAW86369 AAW86369 AAW43571 AAW19706 AAW79684 AAW37827 AAW92439 AAB18766 AAW92439 AAB18766 AAW92439 AAB18766 AAW927020 AAW977020 AAY97021 AAW977021 AAY97021 AAY97021 AAY97022 AAY97021 AAY97022 AAY97023 AAY97026 AAY97027 AAY97027 AAY97027 AAY97028 AAY97028 AAY97028 AAY97028 AAY97028 AAY97028 AAY97027 AAY97028
yer proteins - useful or preparing vaccines									s; spotted fever;						Duroc alpha melano wild boar alpha melan large white alpha- Human MSH-R. Homo Sequence of a poly Melanocortin-1 rec Melanocortin-1 rec Human melanocyte s Human melanocortin Human melan

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                        The alkaline phosphatase (AP) (AAW17830) of Rhodothermus marinus (Rma) has a high pH optimum (10.8) and is thermostable, retaining 60% of its activity after 24 hr at 65 deg. It is also tolerant of other denaturing conditions, such as overnight incubation in 6 M urea at 65 deg. Recombinant AP can be produced in transformed host cells utilising isolated nucleotide sequences (see also AAT66461-63). The properties of the enzyme make it suitable for
                                                                                                                                                                                                                                                                                   Thermostable Rhodothermus marinus alkaline phosphatase enzyme label in immunoassays and nucleic acid assays
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/label- Mat_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-32;
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90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thermophilic enzyme; label; assay.
                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mature protein
21-455 when AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48; I
Pred. No. 0.
        methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprises amino acids is expressed in E. coli "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
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     proteins
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B 8

233

figaiatlt 241

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FIGALATET

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ARESULT ANY34877
ID AAY3
XX AAY3
XX AAY3
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XX AAY3
XX AMIN
XX RESE
KW Sinu
KW Sinu
KW Vacc
OS Chla
XX AO99
PN WO99
XX O4-1
PR 20-1
XX AO1-1
PR 21-1
XX AO2-1
XX AO2-1
CC GEN
XX AAY:
CC Frai
CC Gesp
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Best Local S
Matches 7
Query Match
Best Local S
Matches 8
                                                                                                                                                                      AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, crythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-NOV-1998;
21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine; neutralising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and nucleic acids
                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Griffais R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY34877 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1999-357842/30
Similarity
8; Conserv
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7; Conservative
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  Conservative
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                                                                                                                                  Ā,
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97FR-0014673
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                        69.4%;
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70.0%;
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Pred. No. 48;
                           Score 34;
Pred. No.
core 34; DB red. No. 49; Mismatches
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                                                         20;
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                                                         Length 468;
     Indels
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RESULT
AAG30361
ID AAG:
XX
AC AAG:
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DT 17-0
XX
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AAR04232
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Best Local S
Matches 6
                                                                                                                                                                                                                          Sequencing of the p120 gene showed an ORF starting with ATG at position 226. The ORF has 3900 bp which encode 1300 amino acids resulting in a protein with deduced mol.wt. of 132.611 kb. The amino acid sequence has 31 potential N-glycosylation sites. The other ORF of 726 bp was found about 100 bp downstream and on the opposite strand of the p120 gene. Between the two ORF's is the 106 bp intergenic region which presumably serves as a transcriptional termination site.

The recombinant protein can be used to vaccinate humans against RMSF. The DNA can be used as a hybridisation probe for diagnosis of RMSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gilmore RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Protein
           17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                       Main disclosure is the DNA fragment encoding the 120kb surface protein and the 726bp ORF encoding the 27.6 kD protein, however the specification best available copy is of too poor a quality to produce a beneficial
                                                                                                                                                                                                                                                                                                                                                                                                        Rickettsia rickettsii surface protein gene - used for diagnosis and for producing protein for vaccines against Rocky Mountain Spotted Fever.
                                  AAG30361;
                                                      AAG30361 standard; Protein; 147
                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; ; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1990-139718/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH ) NAT INST OF HEALTH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rickettsia rickettsii R strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rocky Mountain Spotted Fever; vaccine; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rickettsia rickettsii pl20 and 27.6kD surface proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-SEP-1990 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AARO4232 standard; protein; 1267 AA.
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915 fvgaivtd 922
                                                                                                                                                                                                                                                                                                                               index file.
                                                                                                                                2 FIGAIATD 9
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                                                                                                                                                    Similarity 75.06; Conservative
                                                                                                                                                                                                           1267 ·AA;
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                                                                                                                                                               69.4%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                McDonald GA;
                                                                                                                                                    Score 34; DB 11; Pred. No. 1.5e+02; 1; Mismatches 1;
                                                                                                                                                                         Length 1267;
                                                                                                                                                      Indels
                                                                                                                                                    0;
                                                                                                                                                    Gaps
                                                                                                                                                    0
  18-MAY-1999
19-MAY-1999
20-MAY-1999
21-MAY-1999
24-MAY-1999
25-MAY-1999
27-MAY-1999
27-MAY-1999
01-JUN-1999
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110-JUN-1999
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05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
14-MAY-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
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18-JUN-1999;
21-JUN-1999;
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16-APR-1999;
19-APR-1999;
21-APR-1999;
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23-APR-1999;
28-APR-1999;
30-APR-1999;
30-APR-1999;
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05-MAR-1999
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01-APR-1999
06-APR-1999
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18-JUN-1999;
18-JUN-1999;
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18-JUN-1999;
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                                                                         18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
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           990S 0137528.
990S 0137724.
990S 0137724.
990S 0138094.
990S 0139419.
990S 0139453.
990S 0139453.
990S 0139455.
990S 0139456.
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990S 0139458.
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990S-0132485.
990S-0132485.
990S-0132486.
990S-0132466.
990S-0134256.
990S-0134219.
990S-0134219.
990S-0134770.
990S-0134770.
990S-0135124.
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990S-0135639.
990S-0136021.
990S-0136021.
990S-0136021.
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99US-0130510.
99US-0130891.
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99US-0130077
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99US-0128234
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99US-0126785
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AAG30360
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XX
AC AAG3
AC AAG3
AC T17-0
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DE Arab
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XY
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Best Local S
Matches 6
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31-AUG-1999
01-SEP-1999
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11-SEP-1999
22-SEP-1999
23-SEP-1999
24-SEP-1999
24-SEP-1999
25-OCT-1999
07-OCT-1999
Arabidopsis thaliana
                                                                termination
                                                                                   protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                   Arabidopsis
                                                                                                                                                                                                                                                                                                        AAG30360;
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9 tiigavskdt 138
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Similarity 60.0%;
6; Conservative
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                                                             sequence
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Pred. No. 22;
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                                                                                                                                                                                          protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 36281.
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                                                          06-SEP-2000.
                                                                                            EP1033405-A2
                                                                                                                                  Arabidopsis thaliana
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                  25-FEB-2000; 2000EP-0301439.
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144 tiigavskdt 153
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                                                                                                                                                                                                                                                                                                                                                                    standard; Protein;
                                                                                                                                                                        sequence.
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99US-015579

99US-0155486

99US-0155596

99US-0155596

99US-0157717

99US-0158029

99US-0158029

99US-0158232

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99US-0159293

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99US-01614004

99US-0161359

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Pred. No. 24;
2; Mismatches
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08-JUL-1999;
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05-OCT-1999;
06-OCT-1999;
07-OCT-1999;
                                                                                                                     Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; evolutionary study.
                                                           04-JAN-2001.
                                                                                WO200100844-A2
                                                                                                   Corynebacterium
                                                                                                                                                                                                        Corynebacterium glutamicum SMP protein sequence
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161 tiigavskdt 170
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990S-0159293

990S-0159330

990S-0159637

990S-0160741

990S-0160768

990S-0160768

990S-0160815

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990S-0161404

990S-0161404

990S-0161350

990S-0161350
                                                                                                    glutamicum.
                                                                                                                                                                                                                                                                     Protein; 248
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                                                                                                                                                                     metabolism and oxidative phosphorylation (SMP) proteins given in CC AMB79243 to AMB 79633 which are involved in carbon metabolism and CC energy production. The C. glutamicum SMP gene can be used in vectors CC (II) for expression in host cells and production or modulation of cromongrotelinogenic antino acid (preferred), a purine or pyrimidine base, CC or nonproteinogenic antino acid (preferred), a purine or pyrimidine base, CC coloctor, a polyketide, or an eromatic compound, a vitamin, a coffictor, a polyketide, or an eroxyme. The presence of (I) or SMP proteins CC coffictor, a polyketide, or an eroxyme. The presence or activity of CC corpobacterium diphtheriae in a subject. (I), (II), (III) or host cells containing them are used for diagnosing the presence or activity of CC containing them are used to map genomes of organisms related to containing them are used to map genomes of organisms related to containing them are used to map genomes of organisms required containing in modulating SMP protein regions required the metabolism of sugars, and in modulating high-energy molecule production containing in sugars, and in modulating high-energy molecule production
                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Corynebacterium glutamicum nucleic acid encoding a sugar metabolism and oxidative phosphorylation protein for production or modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes -
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; Page 701-702; 1246pp; English.
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N-PSDB; AAF71554.
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99DE-1042123
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                                                        Score 33; DB Pred. No. 39; 1; Mismatches
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RESULT
AAW79067
RESULT 1
AAB41069
ID AAB4
XX
AC AAB4
XX
DT 08-E
XX
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                                                                                                                                                                                                Matches
                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                        The present sequence represents a cytochrome P450 monooxygenase from Sorghum bicolor (L.) Moench, designated P450ox. Cytochrome P450 monooxygenase catalyses: (1) the conversion of aldoxime to a nitrile; and (ii) the nitrile to the corresponding cyanohydrin. DNA encoding cytochrome P450 monooxygenase can be used to obtain transgenic plants, for the purpose of improving the nutritive value or pest resistance of the plant. Cytochrome P450 monooxygenase catalyses the conversion of aldoximes to nitriles to cyanohydrins, which are the precursors of toxic cyanogenic glycosides, so staple food such as cassava and ilma beans, as well as animal feed such as white clover, can be rendered less toxic by blocking the cytochrome P450 monooxygenase activity. Introducing the enzyme to plants or to certain tissues could help reduce crop damage since the product is also toxic to insects, acarids and nematodes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytochrome P450 monooxygenase; P450ox; Sorghum bicolor (L.) Moench; Sinapis alba; biosynthetic conversion; aldoxime; nitrile; cyanohydrin; cyanogenic glycoside; transgenic plant; resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytochrome P450 monooxygenase of the cyanogenic glycoside pathway useful for the production of plants with improved nutritive value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW79067 standard; Protein; 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-520808/44.
N-PSDB; AAV57472.
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07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sorghum bicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-DEC-1998
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                                        AAB41069;
                                                                    AAB41069 standard; Protein; 143
                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Page 41-43; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pest resistance
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tfigaidtss 334
                                                                                                                                                                                               Similarity 7; Conserv
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                                                                                                                                                                                                                                                                     531 AA;
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97EP-0810132.
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                                                                                                                                                                                                             Score 33; DB
Pred. No. 91;
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                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                            Length 531;
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08-FEB-2001

(first entry)

Human ORFX ORF833 polypeptide sequence SEQ ID NO:1666

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; intinunosuppressive; antiinflammatory; antianaemic; gene therapy; cancer; proliferative disorder; hyportension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; considered and considered and

thrombosis; contraceptive.

bone damage; cartilage damage; antiinflammatory disease; coagulation;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC which represent the human ORFX open reading frames 1 to 3161 The ORFX CC sequences have activities such as: cytostatic; hepatotropic; vulnerary; CC antipsoriatic; antiparkinsonian; notropic; neuroprotective; antipsoriatic; anticonvulsant; antiarthritic; immunosuppressant; CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidabetic; hypotensive; dermatological; immunosuppressive; CC antidiabetic; hypotensive; dermatological; antinunosuppressive; CC antitinflammatory; antibacterial; antiviral; antifungal; antirheumatic; CC antithyrold; and antianaemic. The sequences can be used for determining CC the presence of or predisposition to, or preventing or treating CC pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy CC vectors. The proteins and nucleic acids may be used to treat concers, CC proliferative disorders, neurodegenerative disorders, osteoarthritis, CC graft vs host disease, cardiovascular disease, diabetes mellitus, hypothyroldism, cholesterol ester storage, systemic lupus criterias and intertion, malaria, autoimmune disorders, asthma, calletrias and intertion, malaria, autoimmune disorders, asthma, burner symples hore and cartillar damage.
                              Matches 6; Conser
                                                           Query Match
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02-APR-1999;
05-APR-1999;
                                                                                                                                    allergies, aplastic anaemia, burns, wounds, bone and cartil nocturnal haemoglobinuria, antiinflammatory disease; to enh coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 1328; 5507pp; English.
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N-PSDB; AAC75278.
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                                                                                                          Sequence
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 2 FIGAIATD 9
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                                                                                                          143
                                Conservative
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99US-0127728
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                                              65.3%;
75.0%;
                            Score 32;
Pred. No.
1; Mismatc
                              Mismatches
                                              . 34;
                                                         21;
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                                                         Length 143;
                              Indels
                                                                                                                                                    to enhance
                                                                                                                                                                     cartilage
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                              0;
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Sequence

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RESULT 1
ADW 86370
ID AW86370
ID AW86370
XX AW86
XX AW86
XX AW86
XX AW86
XX POIC
KW Giff
KW Giff
KW W Alph
XX W O91
XX W O91
XX W O91
XX W O91
XX A (PI)
XX 
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                                                                                                                                    CC A method has been developed for: (a) differentiating animals and animal CC products according to breed origin; (b) determining or testing the breed CC origin of a product; or (c) validating an animal product. The method CC comprises analysing a sample of the product for the allele(s) of at CC least one breed-determinant (BD) gene. The present invention also CC describes: (1) methods for determining the coat colour genotype of a pig CC hormone receptor (alpha-MSHR) gene; (ii) the amino acid sequence of an CC alpha-MSHR protein at positions associated with coat colour, or the size of the protein; (iii) detecting which microsatelites (or other linked CC marker alleles), linked to the alpha-MSHR gene, or particular alleles of it, are present; and (iv) analysing nucleic acid to determine if the KIT CC gene carries a polymorphism associated with the Belt genotype. The cC mammals, especially pigs, Particular applied to samples from fish, birds and CC mammals, especially pigs, Particular applications are confirming stated CC origin of meats; in quality control; for maintaining stock purity, and CC in the confirment control; for maintaining stock purity, and CC quickly and inexpensively. The process can be made quantitative. The present sequence represents a partial protein sequence of alpha-MSFR CC from a Hampshire breed pig.
                                                  not appear to do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Fig 1; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Differentiating products from different animal breeds - by the analysis of alleles of breed-determinant genes, at the nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
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30-MAY-1997;
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                                                                                                                        Hampshire breed pig
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                                                               do so
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97GB-0011214.
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                                                                                           sequence
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                                                                                           is said to
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                                                                                           AAV80685,
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RESULT 12
AAW86371
IDW AAW863
XX AAW863
XX Duroc
XX Porcin
KW differ
XX Porcin
KW differ
XX WO9854
XX PF 27-MAY
XX PF 27-MAY
XX PF 31-JAN
PR 31-JA
                              cc products according to breed origin; (b) determining or testing the wide configuration of a product, or (c) validating an animal product. The method cc comprises analysing a sample of the product for the allele(s) of at CC least one breed-determinant (BD) gene. The present invention also consists one breed-determinant (BD) gene. The present invention also consists one breed-determinant (BD) gene. The present invention also consists of the supha melanocyte-stimulating controls are consisted for determining the coat colour genotype of a pig commone receptor (alpha-MSHR) gene; (ii) the amino acid sequence of an common acid sequence of an comparation acid sequence of an alpha-MSHR gene, or particular alleles of the protein; (iii) detecting which microsatellites (or other linked common acid sequence of an acid sequence of an acid sequence of an common acid sequence of an acid sequence of acid sequence
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A method has been developed for: (a) differentiating animals and animal products according to breed origin; (b) determining or testing the bree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Fig 1; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or protein level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Differentiating products from different animal breeds - by the analysis of alleles of breed-determinant genes, at the nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-070222/06.
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30-MAY-1997;
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95 flgaiavd 102
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les 6; Conser
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       inexpensively. The process uence represents a partial p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98GB-0001990.
97GB-0011214.
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75.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    red. No. 65;
Mismatches
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       protein
       can be made quantitative. The protein sequence of alpha-MSFR
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CC A method has been developed for: (a) differentiating animals and animal products according to breed origin; (b) determining or testing the breed origin of a product; or (c) validating an animal product. The method comprises analysing a sample of the product for the allele(s) of at least one breed-determinant (BD) gene. The present invention also describes: (l) methods for determining the coat colour genotype of a pig by determining; (i) the allele(s) of the alpha melanocyte-stimulating by determining; (i) the allele(s) of the alpha melanocyte-stimulating alpha-MSHR protein at positions associated with coat colour, or the size of the protein; (iii) detecting which microsatellites (or other linked marker alleles), linked to the alpha-MSHR gene, or particular alleles of the are present; and (iv) analysing nucleic acid to determine if the KIT gene carries a polymorphism associated with the Belt genotype. The main method of the invention is applied to samples from fish, birds and
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Best Local S
Matches 6
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                                                                                                                                                                                                                                                     Differentiating products from different animal breeds - by the analysis of alleles of breed-determinant genes, at the nucleic or protein level
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         porcine; wild boar; meishan; pietrain; large white; hampshire; duroc;
differentiation; breed origin; alpha-MSHR; coat colour; stock purity;
alpha melanocyte-stimulating hormone receptor; KIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wild boar alpha melanocyte-stimulating hormone receptor partial protein
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30-MAY-1997;
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95 flgaiavd 102
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                                                                                                                                                                                                                                                                                                                 AAV80681.
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97GB-0011214.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                       LTD.
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            A method has been developed for: (a) differentiating animals and animal products according to breed origin; (b) determining or testing the breed origin of a product; or (c) validating an animal product. The method comprises analysing a sample of the product for the allele(s) of at least one breed-determinant (BD) gene. The present invention also describes: (1) methods for determining the coat colour genotype of a pig by determining; (i) the allele(s) of the alpha melanocyte-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porcine; wild boar; meishan; pietrain; large white; hampshire; duroc; differentiation; breed origin; alpha-MSHR; coat colour; stock purity; alpha melanocyte-stimulating hormone receptor; KIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mammals, especially pigs. Particular applications are confirming stated origin of meats; in quality control; for maintaining stock purity, and in breeding programmes (to confirm particular crosses). The method requires only very small samples and many samples can be screened quickly and inexpensively. The process can be made quantitative. The present sequence or alpha-MSFR from wild boar.
                                                                                                                                                           Differentiating products from different animal breeds - by the analysis of alleles of breed-determinant genes, at the nucleic or protein level
                                                                                                                                 Claim 12; Fig 1; 101pp; English.
                                                                                                                                                                                                                       WPI; 1999-070222/06.
N-PSDB; AAV80682.
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                                                                                                                                                                                                                                                                                                                                         31-JAN-1998;
30-MAY-1997;
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                                                                                                                                                                                                                                                                                                            (PIGI-) PIG IMPROVEMENT CO UK LTD.
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nes 6; Conserv
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97GB-0011214.
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(alpha-MSHR) gene; (11) the amino acid
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75.0%;
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Pred. No.
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RESULT 1
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N.B. The present sequence is said to be encoded by AAV80682, but does not a mean to do so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Porcine; wild boar; meishan; pietrain; large white; hampshire; duroc; differentiation; breed origin; alpha-MSHR; coat colour; stock purity; alpha melanocyte-stimulating hormone receptor; KIT.
                                                                                                                                                               Differentiating products from different animal breeds - by the analysis of alleles of breed-determinant genes, at the nucleic
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30-MAY-1997;
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A method has been developed for: (a) products according to breed origin; (

(b) differentiating animals and (b) determining or testing tl

nd animal the breed

Claim 12;

Fig 1;

101pp;

English

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Search completed: September 28, 2001, 12:26:03 Job time: 7339 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cc origin of a product; or (c) validating an animal product. The method cc comprises analysing a sample of the product for the allele(s) of at cleast one breed-determinant (BD) gene. The present invention also cc describes: (1) methods for determining the coat colour genotype of a pig CC by determining; (i) the allele(s) of the alpha melanocyte-stimulating CC by determining; (ii) the allele(s) of the alpha melanocyte-stimulating CC alpha MSHR protein at positions associated with coat colour, or the size of the protein; (iii) detecting which microsatellites (or other linked CC marker alleles), linked to the alpha-MSHR gene, or particular alleles of it, are present; and (iv) analysing nucleic acid to determine if the KIT gene carries a polymorphism associated with the Belt genotype. The CC mammals, especially pigs. Particular applications are confirming stated CC origin of meats; in quality control; for maintaining stock purity, and in breeding programmes (to confirm particular crosses). The method CC origin of meats; want is amples and many samples can be screened CC quickly and inexpensively. The process can be made quantitative. The present sequence represents a partial protein sequence of alpha-MSFR CC from a Large White breed pig.

CC N.B. The present sequence is said to be encoded by AAV80684, but does on the sequence of alpha-MSFR control of the present sequence is said to be encoded by AAV80684, but does on the sequence is said to be encoded by AAV80684, but does on the sequence is said to be encoded by AAV80684, but does on the sequence is said to be encoded by AAV80684, but does on the sequence is said to be encoded by AAV80684, but does on the sequence is said to be encoded by AAV80684, but does on the sequence is said to be encoded by AAV80684, but does on the sequence is said to be encoded by AAV80684, but does on the sequence is said to be encoded by AAV80684, but does on the sequence is said to be encoded by AAV80684, but does on the sequence is said to be encoded by AAV80684, but does on the seque
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Best Local Similarity 75.0
Matches 6; Conservative
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Listing first 45 summaries
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Perfect score:
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1: /cgnl_7/ptodata/1/1aa/5A_COMB.pep:*
2: /cgnl_7/ptodata/1/1aa/5B_COMB.pep:*
3: /cgnl_7/ptodata/1/1aa/6B_COMB.pep:*
4: /cgnl_7/ptodata/1/1aa/6B_COMB.pep:*
5: /cgnl_7/ptodata/1/1aa/backfilesl.pep:*
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Gapop 10.0 , Gapext 0.5
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 Query Match
Best Local Similarity
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RESULT 1 US-08-169-927-2 Sequence 2, Applia Patent NO. 578344 GENERAL INFORMAT APPLICANT: Cal APPLICANT: Chal APPLICATI NO COUNTRY: Bether STATE: MD COUNTRY: Bether STATE: MD COUNTRY: US- COMPUTER READAN MEDIUM TYPE: COMPUTER: CAL SOFTWARE: READAN MEDIUM TYPE: CLASSIFICATION I FILING DATE: CLASSIFICATION I FILING APPLICATION I FILING DATE: CLASSIFICATION I APPLICATION I APPLICA	
pplication 83441 RMATION: Carl, Mit Carl, Mit Dobson, M Ching, Me Ching, Me Ching, Me Ching, Mit Dobson, M Carlon: SEQUENCE ADDRES E: Counsel Bldg: NVENTION: NUMBER: Flopp: FLICATION: FLICATIO	88 8 5 5 7 7 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
699 A A A A A A A A A A A A A A A A A A A	120 5 PCT-1 120 5 PCT-1 120 5 PCT-1 189 1 US-0 295 2 US-0 295 2 US-0 364 3 US-0 364 3 US-0 377 2 US-0 77 2 US-0 77 2 US-0 236 3 US-0
	-US93-11292-1 -US95-06918-1 08-709-912-13 08-464-517-2 08-464-517-2 08-464-6-3 08-463-772-2 08-582-740-70 08-582-740-70 08-582-740-70 08-582-140-70 08-582-140-70 08-582-140-70 08-582-140-70 08-582-140-70 08-582-140-70 08-582-140-70 08-582-140-70 08-582-140-70 08-582-140-70 08-582-140-70 08-582-140-70 08-683-13 08-343-4438-13 08-343-4438-13 08-343-4438-13 08-343-4438-13 08-343-4438-13 08-343-4438-13 08-343-4438-13 08-343-4438-13 08-343-4438-13
of Both	Sequence 1, Appli Sequence 1, Appli Sequence 13, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 68, Appli Sequence 25, Appli Sequence 25, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli

98.0%;

Score 48; Pred. No.

DB 1; 0.14;

Length 1612;

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GENERAL INFORMATION:
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CLASSIFICATION:
PRIOR APPLICATION NUMBER: 60/005,965
APPLICATION NUMBER: 69/465,003
PRIOR APPLICATION NUMBER: 09/465,003
PRIOR TOATION NUMBER: 1995
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FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/575,354
FILING DATE: December 20, 1995
APPLICATION NUMBER: 08/240,158
FILING DATE: May 10, 1994
APPLICATION NUMBER: 08/229,329
FILING DATE: APT11 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Marbirg 8:65474,1
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                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 455 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
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STATE: Calle
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STREET: 633 West Fifth Street
STREET: Suite 4700
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TELEX: (213) 955-0440
TELEX: 67-3510
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REFERENCE/DOCKET NUMBER: 222/158
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warburg, Richard J.
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Davis, Maria
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70.0%;
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Query Match
Best Local Similarity
"hehes 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                    US-08-671-525B-2
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TELEFAX: 312-715-1234
TELEX: 910-721-5317
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08671525B Patent No. 5703220
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APPLICATION NUMBER: US/07/866
FILING DATE: 19920410
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5532347nan, Kevin E
REGISTRATION NUMBER: 35,303
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
CITY: Bloomfield Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                              APPLICANT: Yamada, APPLICANT: Gantz, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cone, Roge APPLICANT: Mountjoy, TITLE OF INVENTION: & TITLE OF INVENTION: &
                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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CITY: Chicago
STATE: Illinoi:
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                                                                                                          ZIP: 48303
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10 South Wacker Drive, Suite 3000
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75.0%;
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Pred. No. 41;
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                      Version #1.25
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US/08/671,525B

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                                 Query Match
 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (810)641-027 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                         TELEFAX: (810)641-0270 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acid
                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                                                                                                                         TELEPHONE: (810)641-1600
Local Similarity hes 6; Conserv
                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/672,109B FILING DATE: June 27, 1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Harness, Dickey & Pierce, P.L.C
STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: MI
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                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 48303
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                          317 amino acids
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 Conservative
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                  65.3%;
75.0%;
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75.0%;
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Pred. No.
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                  Score 32;
Pred. No.
   Mismatches
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                                 DB 1;
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                                 Length 317;
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Best Local S
Matches 6
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APPLICANT: Yamada,
APPLICANT: Gantz, I.
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5817787
                                                                                                                                                                                                                      Sequence 6, Application US/08466906B Patent No. 5849871
                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (810)641-0270 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                   APPLICANT: Cone, Roger
APPLICANT: Mountjoy, K
TITLE OF INVENTION: ME
TITLE OF INVENTION: at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
COMPOTER: PERM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/842,045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Harness, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810)641-1600
                                                                                                         NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 36683
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                   134 FLGAIAVD 141
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nes 6; Conserv
                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid TOPOLOGY: linear
                           COUNTRY:
                                                           CITY: Chicago
                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Bloomfield Hills
                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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                                                                           E: McDonnell Boehnen Hulbert & Berghoff 300 South Wacker Drive
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                               USA
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                                                                                                                                           and Uses
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75.0%;
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                                                                                                                                                         Stimulating Hormone Receptor
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MOLECULE TYPE: protein .-08-842-238-2
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ATTORNEY/AGENT INFORMATION:
NAME: NO. 5849871nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,154-H
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
                                                   TELEFAX: (810)641-0270
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 2115-000853DVD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810)641-1600
                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,238
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yamada, Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: MI
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 312-913-0002
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                                       TOPOLOGY:
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                                         linear
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75.0%;
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US-08-706-281A-6

; Sequence 6, Application US/08706281A

; Patent NO. 6100048

; GENERAL INFORMATION:
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; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-780-749A-4
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US-08-780-749A-4
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Best Local Similarity /J...
Change 6; Conservative
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Best Local S
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OPERATING SYSTEM: DOS
SOFTWARE: FBSTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,7
FILING DATE: 08-JAN-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 869-8864/y.
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Laura A. COTUZZI
REGISTRATION UNMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
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APPLICANT: Huszar, Dennis
APPLICANT: Gu, Wei
TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS
TITLE OF INVENTION: USEFUL IN THE REGULATION OF BODY WEIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
APPLICANT:
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                                                                                                                                                         134 FLGAIAVD 141
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ZIP: 10036/2711
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es 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                amino acids
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                              E: (212) 790-9090
(212) 869-8864/9741
           Cone, Ro
Boston, Bruce A
                            Roger D
                                                                                                                                                                                                                                      65.3%;
75.0%;
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75.0%;
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    Mismatches

                                                                                                                                                                                                                                      Score 32; DB
Pred. No. 41;
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Pred. No. 41;
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                                                                                                                                                                                                                                                       DB 2; Length 317;
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US-08-629-335B-2
; Sequence 2, Application US/08629335B
; Patent No. 6117975...
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                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,281A
FILING DATE: 04-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chen, Wen
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6100048nan, Kevin
REGISTRATION NUMBER: 35,303
                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                         APPLICANT: Yamada, Tadataka
APPLICANT: Gantz, Ira
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                                                                                                                                                                                                                                                                                                       ITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 75.0
                                                                                                                                                   COUNTRY: U
                                                                                                                                                                                        CITY: Bloomfield Hills STATE: MI
                                                                                                                                                                                                                             STREET:
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ZIP: 60606
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APPLICATION NUMBER: US/08/629,335B
FILING DATE: July 23, 1996
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300 South Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                   Genes Encoding Melanocortin Receptors
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kevin E
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Pred. No.
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Best Local Similarity
Query Match
Best Local Similarity
""" 6; Conserve
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US-09-201-746-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (810)641-0270 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cone, Koyer L
APPLICANT: Mountjoy, Kathleen G
TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6268221nan, Kevin
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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NAME: Smith, DeAnn F.
REGISTRATION NUMBER: 366
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                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                     TELEFAX:
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                                                                                                                                            LENGTH:
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                                                                                                                            amino acid
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               Conservative
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75.0%;
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75.0%;
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                                                                                                                                                                                                                                                                              Kevin E
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                           Score 32;
Pred. No.
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Pred. No.
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41;
                                          DB 4;
                                         Length 317;
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               Indels
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FIGAIATD 9

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Matches
                                                                                                                        Sequence 1, Application US/09352619
Patent No. 6084070
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 650-855-0555
TELEPAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MUENZEN, COLETTE C.
REGISTRATION NUMBER: 39,784
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                   APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN GLUTAREDOXIN BETA
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
LIBRARY: THP1N
CLONE: 2447829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/911,319A FILING DATE: AUGUST 14, 1997 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: COCley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN GLUTAREDOXIN BETA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                      129 TFIGG-ATDT 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 amino acids
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Pred. No. 41;
0; Mismatches
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; CLONE: 2447829
US-09-352-619-1
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Best Local Similarity
""hhes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                             GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/352,619
FILING DATE:
                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER RÉADABLE FORM:
MEDIUM TYPE: Diskett
          APPLICATION NUMBER: US/08/973,461A FILING DATE: 20-APR-1998 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                      SOFTWARE: PatentIn CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                            STREET: 1,55
CITY: ARLINGTON
                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 TFIGG-ATDT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3174 POI
CITY: Palo Alto
                                                                                                                                                                COUNTRY: U
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 39,7 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
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APPLICATION NUMBER:
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Copyright (c) 1993 - 2000 Compugen Ltd.
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## ALIGNMENTS

JN0896

N;Alternate names: cell surface antigen scap; paracrysturint the control of mitochondria.

N;Contains: 32K beta peptide
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 03-Nov-2000
C;Accession: D71630; A36473
C;Accession: D71630; A36473
C;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
Nature 396, 133-140, 1998
Nature 396, 133-140, 1998 A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1645 <HAH>
A; Residues: 1-1645 <HAH>
A; Residues: 1-1645 <HAH>
A; Residues: 1353-1371 <HA2>
F; Residues: 1353-1371 <HA2>
F; Residues: Res C:Species: Rickettsia typhi
C:Species: Rickettsia typhi
C:Species: Rickettsia typhi
C:Date: 19-May-1994 #sequence\_revision 19-May-1994 #sext\_change 28-May-1999
C:Date: 19-May-1994 #sequence\_revision 19-May-1994 #sext\_change 28-May-1999
C:Accession-30,0896; PNO686
R-HSIN, M.J.: Kim, K.K.; Kim, I.; Chang, W.H.
Gene 133, 129-133 A:Molecule type: DNA
A;Residues: 1-1643 <AND>
A;Residues: 1-1643 <AND>
A;Cross-references: GB:AJ235273; GB:AJ235269; NID:g3861237; PIDN:CAA15140.1; PID:e134
A;Cross-references: GB:AJ235273; GB:AJ235269; NID:g3861237; PIDN:CAA15140.1; PID:e134
A;Experimental source: strain Madrid E
R;Carl, M.; Dobson, M.E.; Ching, W.M.; Dasch, G.A.
R;Carl, M.; Dobson, M.E.; Ching, W.M.; Dasch, G.A.
Proc. Natl. Acad. Sci. U.S.A. 877, 8237-88241, 1990
A;Title: Characterization of the gene encoding the protective paracrystalline-surface
A;Reference number: A36473; MUID:91045972 A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria A;Reference number: A71630; MUID:99039499
A;Accession: D71630 outer membrane protein B precursor - Rickettsia prowazekii N;Alternate names: cell surface antigen sca5; paracrystalline surface-layer protein; RESULT D71630 В Qγ A; Status: nucleic acid sequence not shown; translation not shown Matches Query Match Best Local Similarity 1296 1 TFIGAIATDT 10 TFIGALATET 1305 10; Conservative 100.0%; .08; 0; Score 49; Pred. No. Mismatches 0.09; DB 2; gene encoding the crystalline surface 0 Length 1645; Indels predicted <MAT> 0 Gaps 0

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R; Knnst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallezi icch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schielich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serorakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchlyama, T.; Winters, P.; Mipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Althors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A.;Authors: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A.; Accession: D70035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A36473
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 33-177, 'VC', 180-190, 'INSRSSSYHLVS', 202-211, 'I', 213-256, 'A', 258-312, 'L', 314-1
A; Cross-references: GB:M37647; NID:g152497; PIDN:AAA26390.1; PID:g152498
A; Note: the authors translated the codon AAT for residue 146 as Ala, CGT for residue 478
5 is inconsistent with the translation of the nucleotide sequence
A; Note: parts of this sequence were determined by protein sequencing
R; Hackstadt, T.; Messer, R.; Cieplak, W.; Peacock, M.G.
Infoct. Immun. 60, 159-165, 1992
A; Title: Evidence for proteolytic cleavage of the 120-kilodalton outer membrane protein
A; Reference number: A43869; MUID:92104668
A; Contents: annotation
RESULT 4
S07575
Outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: strain C:Genetics: A; Gene: yveA
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F;2-1352/Product: outer membrane protein B #status predicted <MATO>
F;1353-1643/Product: 32K beta peptide #status experimental <MATB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             permease homolog yveA - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:Z99121; GB:AL009126; NID:g2635827; PIDN:CAB15452.1; PID:g2635960
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A; Residues: 1-520 <KUN>
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C;Species: Rickettsia rickettsii
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 05-Dec-1998
C;Accession: S07575; S18579; A43869
R;Gilmore Jr., R.D.; Joste, N.; McDonald, G.A.
McDonald, 3, 1579-1586, 1989
A;Title: Cloning, expression and sequence analysis of the gene encoding the A;Reference number: S07575; MUID:90136087
A;Accession: S07575
                                                                                                                                                                                                                                                                                                                                                                                                                                                        outer membrane protein B precursor - Rickettsia japonica C;Species: Rickettsia japonica C;Date: 30-Sep-1993 #sequence_revision 21-Jan-1997 #text_change 13-Nov-1998 C;Accession: JC1340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Hackstadt, T.; Messer, R.; Cieplak, W.; Peacock, M.G.
Infect. Immun. 60, 159-165, 1992
A;Title: Evidence for proteolytic cleavage of the 120-kilodalton outer membrane prote A;Reference number: A43869; MUID:92104668
A;Accession: A43869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Gilmore, R.D.; Joste, N.; McDonald, G.A. Mol. Microbiol. 5, 3089, 1991
A;Reference number: S18579; MUID:92236427
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                                                                                                                                                      C:Keywords: membrane protein
F:1-34/Domain: signal sequence #status
F:35-1651/Product: outer membrane prote
                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-1651 < YAN>
                                                                                                                                                                                                                                                                                                                                            A; Reference number: JC1340
A; Accession: JC1340
                                                                                                                                                                                                                                                                                                                                                                                      R;Yan, Y.; Uchida, T.
Chinese J. Microbiol. Immunol. 16, 220-226, 1996
A;Title: Cloning and sequence analysis of the gene encoding the 120kDa outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Keywords: glycoprotein
F;2-1007/Product: outer membrane protein B *status predicted <MATO>
F;1008-1300/Product: 32K beta peptide *status experimental <MATB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Note: sequence extracted from NCBI backbone (NCBIP:74388) and corrected
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A; Residues: 994-1004 <GIL2>
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A; Accession: S18579
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A; Residues: 1-994, 'DLKLEH', 1001, 'GS', 1005-1300 <GILL>
A; Cross-references: EMBL: X16353
                                                             Query Match
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Best Local
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                                            Similarity 7; Conserv
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7; Conserv
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77.8%;
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77.8%;

    Mismatches

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Pred. No. 11;
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A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler ietch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, F.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seroyakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchlyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A; Reference number: A69580; MUID:98044033

A; Reference number: A69580; MUID:98044033
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A; Status: preliminary
A; Molecule type: DNA
A; Roslidues: 1-174 < HIB>
A; Roslidues: 1-174 < HIB>
A; Roslidues: GB: M19075; NID: g155973; PIDN: AAA27830.1; PID: g155977
A; Cross-references: GB: M19075; NID: g155973; PIDN: AAA27830.1; PID: g155977
probable phosphatidate cytidylyltransferase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
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A; Accession: A45937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          early chorion protein 5H4 precursor - silkworm C;Species: Bombyx mori (silkworm) C;Decies: Bombyx mori (silkworm) C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 20-Aug-1999 C;Accession: A45937
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A;Experimental source: strain 168
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A; Residues: 1-344 <KUN>
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C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
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C;Date: 05-Dec-1997 #sequence_revision
C;Accession: H70030
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70.0%;
                                                                                                                                                                                                                                                                                                              73.5%;
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Pred. No. 4.5;
2; Mismatches
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A;Cross-references: G
C;Genetics:
A;Gene: At2g45150
A;Map position: 2
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A; Residues: 1-2434 <WIL>
A; Cross-references: EMBL:L07144; NID:g156412; PID:g156413
C; Genetics:
A; Introns: 32/3; 128/3; 361/3; 506/1; 710/3; 1000/2; 1045/3; 1221/2; 1294/1; 1378/2;
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487
A;Accession: A84887
A;Status: preliminary
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987
A;Accession: F70937
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                       hypothetical protein Rv2188c - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: F70937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA topoisomerase II - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change
C;Accession: S44861
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A; Accession: S44861
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A; Residues: 1-430 <STO>
A; Molecule type: DNA
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66.7%;
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2; Mismatches
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references: GB:AL021957;

GB:AL123456; NID:g3242293; PIDN:CAA17492.1;

PID: g291

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amino acid transporter [imported] - Chlamydophila pneumoniae (strain J138) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C;Accession: B86526 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, Nucleic Acids Res. 28, 2311-2314, 2000 A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138. A;Reference number: A86491; MUID:20330349 A;Accession: B86526
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A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255
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C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C; Accession: D72097; A81573
R; Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999
A; Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A; Reference number: A72000; MUID:99206606
A; Accession: D72097
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C; Genetics:
A; Gene: Rv2188c
C; Superfamily: probable
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C;Superfamily: L-lysine transport protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-468 <ARN>
A;Cross-references: GB:BA000008;
A;Experimental source: strain J13
                                                  A; Molecule type: DNA
A; Residues: 1-468 <STO>
                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-468 < REA>
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Best Local
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8; Conserv
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                         NID:g8978656; PIDN:BAA98492.1; GSPDB:GN00142
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Pred. No. 28;
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Pred. No. 33;
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eologis, A.; Ecker, J.R.
submitted to the EMBL Data Library, January 1998
A;Description: Genomic sequence for Arabidopsis thaliana
A;Reference number: Z14208
A;Accession: T00893
                                                                                                                                                                                                                                                                                                                                                                                                                                   probable membrane protein ycdZ - Escherichia coli
C;Species: Escherichia coli
C;Species: - Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
C;Accession: A64846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Introns: 76/1
C;Superfamily: thioredoxin; thioredoxin homology
C;Keywords: redox-active disulfide
C;Keywords: redox-active disulfide
F;82-165/Domain: thioredoxin homology <TXN>
F;104-107/Disulfide bonds: redox-active #status predicted
                                      F:19-35/Domain: transmembrane #status predicted <TM1>F:37-53/Domain: transmembrane #status predicted <TM2>F:68-84/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                            A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74120.1; PID:g17872
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                             Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: A64846
                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: A64846
R; Blattner, F.R.; Plunkett III,
A.; Rose, D.J.; Mau, B.; Shao,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, eologis, A.; Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thioredoxin F21B7.7 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 05-May-2000
                                                                                                           A;Gene: ycdZ
C;Keywords: transmembrane protein
                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-179 <BLAT>
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A; Residues: 1-179 <SI
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                                                                                                                                                                                                                                                                          A; Status: nucleic
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Similarity 60.0%;
6; Conservation
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8; Conserv
                transmembrane #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                          G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, Y.
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Pred. No.
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Pred. No. 33;
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predicted
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19;
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hypothetical protein ycdz [imported] - Escherichia coli (strain 0157:H7)
c;Species: Escherichia coli
c;Species: Escherichia coli
c;Cspecies: Escherichia coli
c;Cspecies: Escherichia coli
c;Caccession: B85665
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85665
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-179 <STO>
A;Cross-references: GB:AE005174; NID:g12514565; PIDN:AAG55782.1; GSPDB:GN00145; UWGP:216
A;Experimental source: strain 0157:H7, substrain EDL933
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Search completed: September 28, 2001, 12:27:10 Job time: 7255 sec
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                                                                                                                                                                                                               Query Match 67.3%;
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 67.3
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                    1 TFIGALAT 8
||||| ||
123 TFIGACAT 130
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123 TFIGACAT 130
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87.5%;
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Pred. No. 19;
0; Mismatches 1; Indels
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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length:
   protein search, using sw model
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Match
 US-09-551-645-1
49
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Gapop 10.0 , Gapext 0.5
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1300
1654
 YCDZ_SATY
YCDZ_SATY
YCDZ_ECOLI
DHBD_ASPND
GORBI
CTEL_SORBI
HIS5_EMENI
CHCC_ANTPO
MSHR_BOVIN
MSHR_CAPCA
MSHR_STAAU
PCCAPH_STAAU
PCCAPH_
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CHCB_BOMMO
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                                       p34544 caenorhabdi
006653 r outer mem
054290 salmonella
048737 arabidopsis
p75916 escherichia
p80346 aspergillus
048958 sorghum bic
099499 emericella
p80390 antheraea p
447798 bos taurus
077616 canis famil
p56444 capra hircu
p56445 cervus elap
p56446 dama dama (
001726 homo sapien
p56447 rangifer ta
019037 ovibos mose
p56448 rangifer ta
019037 ovibos taries
029154 vulpes vulp
p39857 staphylococ
p22259 escherichia
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32 KDA BETA PEPTIDE.

29 MEMBRANE ANCHOR (POTENTIAL).

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G -> S (IN REF. 7).
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Hackstadt T., Messer R., Cieplak W. Jr., Peacock
"Evidence for proteolytic cleavage of the 120-ki
membrane protein of ricketsiae: identification
Gilmore R.D. Jr., Joste N., McDonald G.A.;

"Cloning, expression and sequence analysis of the gene encoding
120 kD surface-exposed protein of Rickettsia rickettsia.";

MOI. Microbiol. 3:1579-1586(1989).

-I- FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS
RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTI-
-I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED B
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EUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETISIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE SURCELJURAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED SUBCELLURAR LOCATION: CELL WALL.
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V -> A (IN STRAIN BREINL).

Y -> D (IN STRAIN BREINL).

A -> S (IN STRAIN BREINL).

AA -> VC (IN REF. 1).

TTOEAPLTLGA -> INSRSSSYHLVS (IN REF. 1).

T -> I (IN REF. 1).

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           Rickettsia rickettsii
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MISCELLANDEOUS: ITS C-TERMINUS POTENTIALLY MAY BEAR THE EPITOPES CONFERRING ANTIGENICITY TO THE PROTEIN.
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Best Local S
Matches 7
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SEQUENCE
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                        "Organization and expression chorion locus."; pev. Biol. 125:423-431(1988).
                                                                  SEQUENCE FROM N.A. MEDLINE-88112521; Hibner P.
                                                                                                                         Bombyx mori (Silk moth).
Eukaryota; Metazoa; Arthropoda;
Pterygota; Neoptera; Endopterygo
Bombycoidea; Bombycidae; Bombyx.
                                                                                                                                                                             CHCB_BOMMO STANDARD; PRT; 174 AA. P08830; 01-NOV-1988 (Rel. 09, Created) 01-JAN-1990 (Rel. 13, Last sequence update) 01-FEB-1991 (Rel. 17, Last annotation update) CHORION CLASS CB PROTEIN M5H4 PRECURSOR.
                                                                                                                                                                                                                                                                                                              1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning, expression and sequence analysis of the gene encoding surface-exposed protein of Rickettsia rickettsii."; Mol. Microbiol. 3:1579-1586(1989).

-i- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETISIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

-i- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The 120 kilodalton outer membrane protein (rOmp B) of Ri
rickettsii is encoded by an unusually long open reading f
evidence for protein processing from a large precursor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia. NCBI_TaxID=783; [1]
SEQUENCE OF 6-174 FROM
                                                                                                             NCBI_TaxID=7091;
                                                                                                                                                                                                                                                            OMMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X16353; CAA34403.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
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Gilmore R.D. Jr.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gilmore R.D.
                                                                Hibner B.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 279-1654 FROM N.A:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92167802;
Gilmore R.D. Jr.,
                                                                                                                                                                                                                                                                                                                                      N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Event European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content if if and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                              FVGAIVTDT 1310
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                                                                                                                                                                                                                                                                                                                                                              Similarity 77.8
7; Conservative
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1181 11
1654 AA;
                                                                Burke W.D.,
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Cieplak W. Jr.,
                                                  expression of
                                                                          PubMed=3338621;
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1188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=2515418;
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77.8%;
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lae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               wall.
                                                                Lecanidou
                                                                                                                                                                                                                                                                                                                                                              ; Score 39; DB; Pred. No. 5.4; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 KDA SURFACE-EXPOSED 32 KDA BETA PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-THR
                                                                                                                                         Tracheata; Hexapoda; Insecta; ota; Lepidoptera; Glossata; Ditrysia;
                                                    three
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                                                    the
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) of Rickettsia
                                                    Eickbush
silkmoth
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Best Local
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                          Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A. Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Johnston B., O'Callaghan M., Parsons J., Egyd C., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Mounders D., Shownkeen J. Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R., Sulston J., Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                P34544;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
HYPOTHETICAL 142.5 KDA PROTEIN R05D3.11 IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eggshell;
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M19075; AAA27839.1; -.
EMBL; M13835; AAA27829.1; -.
PIR; B23548; B23548.
PIR; A45937; A45937;
HSSP; P00588; IDTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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 Waterson R., Watson Wohldman P.; "2.2 Mb of contiguou
                                                                                                                                                                                   STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             R05D3.11
                                                                                                                                                                                                                                                                                                                                                                                                                    CAEEL
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Pfam; PF01723; Chorion; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. -1- FUNCTION: THIS PROTEIN IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA and CB.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lecanidou R., Rodakis G.C., Eickbush T.H., Kafatos revolution of the silk moth chorion gene superfamil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-86313609; PubMed-3462711;
Lecanidou R., Rodakis G.C., Eickb
                                                                                                                                                                                                                                               NCBI_TaxID=6239;
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nes 6; Conserv
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 contiguous
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71
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   nucleotide
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CENTRAL DO
RIGHT ARM.
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ONE OF MANY FROM TI
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B0ED1BC8928CC568
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2.3;
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    chromosome
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RESULT 7
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30-MAY-2000
30-MAY-2000
01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
OUTER MEMBRANE PROTEIN B PRECURSOR (168 KDA SURFACE-LAYER PROTEIN)
(SURFACE PROTEIN ANTIGEN) (CELL SURFACE ANTIGEN) (SCA5) (ROMP B)
[CONTAINS: 120 KDA SURFACE-EXPOSED PROTEIN (SURFACE PROTEIN ANTIGEN)
(120 KDA OUTER MEMBRANE PROTEIN OMPB); 32 KDA BETA PEPTIDE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01429; MBD; 1.
Pfam; PF00856; SET; 1.
PROSITE; PS50280; SET; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             elegans.";
Nature 368:32-38(1994).
-!- SIMILARITY: CONTAINS 1 SET DOMAIN.
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WormPep; R05D3.11; CE00529.
                         entities requires a license agreement (sor send an email to license@isb-sib.ch).
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                                                                                          the
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                                                                                                                                                                                                                               Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
-I- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A P
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKET
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OMPB_RICJA
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                                                             modified
                                                                                                         between
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=35790;
                                                                                                                                                                                                                                                                                                                                                                                                         Rickettsiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Rickettsia japonica
                                                                                                                                                                                                                                                                                                                               Jchiyama
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                              )aponica."
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                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                   (BY SIMILARITY).
SUBCELLULAR LOCATION: CELL WALL.
                                                                                                                                                                                                    SIMILARITY).
FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS
                                                                                                                                                        LAYER WITH HEXAGONAL SYMMETRY.
AB003681;
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                                                          non-profit institutions as long and this statement is not removed
                                                                                                                                                                                                                                                                                                             of the gene encoding the protein rOmp B of Rickettsia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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BAA20138.1;
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                                              http://www.isb-sib.ch/announce/
                                                          Usage
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Matches 7; Conserv
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Best Local
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SEQUENCE
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                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                          Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium
Escherichia coli with respect to operon structure and regulation.
J. Bacteriol. 180:722-731(1998).
                                 ARATH
                                                                                                                                                                                                                         Hypothetical
                                                                                                                                                                                                                                           EMBL; AJ002301; CAA05311.1; -. StyGene; SG10739; ycdz.
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40, Last annotation update)
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YCDZ_ECOLI
P75916;
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01-NOV-1997
30-MAY-2000
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EMBL; AC002560; AAF85525.1; -.
HSSP; P00274; 1Trp.
Mendel; 27907; Arath;1238;27907.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C., Khan S., Brooks S., Buehler E., Chin C., Chiou J., Choi E., Conn L., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn E., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J. Conway A., Gonzales A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Poriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20047910; PubMed=10580150; Mestres-Ortega D., Meyer Y.; "The Arabidopsis thaliana genome encodes at and a new prokaryotic-like thioredoxin."; Gene 240:307-316(1999).
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                                                                            ECOLI
                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00085; thiored; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases -i- FUNCTION: PARTICIPATES IN VARIOUS REDOX REACTIONS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brassicales;
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161 TIIGAVSKDT 170
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6; Conserv
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(Rel.
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CHLOROPLAST PRECURSOR (
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THIOREDOXIN M-TYPE 1.
REDOX-ACTIVE (BV SIMILARITY).
3589E7C1D132F492 CRC64;
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                                                                    DHBD_ASPNG STANDARD; PRT; 292 AA.
PB0346;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
0-PYROCATECHUATE DECARBOXYLASE (EC 4.1.1.46) (2,3-DIHYDROXYBENZOIC
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STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
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D90740; BA
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Figure 1 refer Fransmembrane.

Forein; Transmembrane.
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CYTOCHROME P450 71E1 (EC
CYP71E1.
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Best Local
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C7E1_SORBI
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

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SETAIN-CV. SS1000; TISSUE-Etiolated seedling;

MEDLINE-98145474; PubMed-9484480;

MEDLINE-98145474; PubMed-9484480;

Bak S., Kahn R.A., Nielsen H.L., Moeller B.L., Halkier B.A.;

Bak S., Kahn R.A., Nielsen H.L., Moeller B.L., CYP71E1, CYP98, and CYP99

"Cloning of three A-type cytochromes P450, CYP71E1, CYP98, and CYP99

"Cloning of three A-type cytochromes p450, CYP71E1 and identification from Sorghum bicolor (L.) Moench by a PCR approach and identification by expression in Escherichia coli of CYP71E1 as a multifunctional by expression in Escherichia coli of CYP71E1 as a multifunctional by expression in the biosynthesis of the cyanogenic glucoside
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NON_CONS
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Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Asperg
NCBI_TaxID-5061;
                                                                                                                                                                                                                                        Sorghum bicolor (Sorghum)
Eukaryota; Viridiplantae;
Magnoliophyta; Liliopsida;
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"2,3-Dihydroxybenzoic acio
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                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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230:104-110(1995).
TIVITY: 2,3-DIHYDROXYBENZOATE - CATECHOL + CO(2).
TOTAL THE METABOLISM OF INDOLE TO CATECHOL.
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Embryophyta; Tracheophyta; Sp.; Poales; Poaceae; PACC clade;
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annotation
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Plant Mol. Biol. 36:393-405(1998).

-I- FUNCTION: CATALYZES THE CONVERSION OF P-HYDROXYPHENYLACETALDOXIME

TO P-HYDROXYMANDELONITRILE. THE DEHYDRATION OF THE OXIME TO THE

CORRESPONDING NITRILE IS FOLLOWED BY A C-HYDROXYLATION OF THE

NITRILE TO PRODUCE P-HYDROXYMANDELONITRILE.

-I- PATHWAY: BIOSYNTHESIS OF THE CYANOGENIC GLUCOSIDE DHURRIN.

-I- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM
                                                                         Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: CATALYZES AN AMIDOTRANSFERASE REACTION THAT GENERATES IMIDAZOLE-GLYCEROL PHOSPHATE AND 5-AMINOIMIDAZOL-4-CARBOXAMIDE RIBONUCLEOTIDE, WHICH IS USED FOR PURINE SYNTHESIS.

-!- FUNCTION: CATALYZES THE CYCLIZATION REACTION THAT PRODUCES D-ERYTHRO-IMIDAZOLE GLYCEROL PHOSPHATE.

-!- PATHMAY: FIFTH AND SIXTH STEPS IN HISTIDINE BIOSYNTHETIC PATHMAY.
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE HISH FAMII-1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE HISH / HIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9P4P9;
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
BIFUNCTIONAL HISTIDINE BIOSYNTHESIS PROTEIN HISHF [INCLUDES: HISH-TYPE AMIDOTRANSFERASE (EC 2.4.2.-); HISF-TYPE CYCLASE].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eurotiales; Trichocomaceae;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
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PROSITE; PS00086; CYTOCHROME_P450; 1.
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InterPro; IPR002401; -
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the European Bioinformatics Institute
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SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                             SIMILARITY:
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Similarity 70.0%;
7; Conservative
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531 AA;
                                                                                                                                                                                                                                                                                                                                                                                            Draht O.,
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                       CONTAINS
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                                                                                                                                                                                                                                                                                                                                                               HOffmann B., Kuebler E., Braus G.H.; erization of the hisHF gene of Asperg
                       1 TYPE-1
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l; Mismatches
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2272E4AA910890D2
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                 GLUTAMINE
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Pfam; PF01723; Chorion; 1.

Chorion;

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                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comparison of C and B family sequences.";
Proc. Natl. Acad. Sci. U.S.A. 80:1043-1047(1983).
-!- EUNCTION: THIS PROTEIN IS ONE OF MANY FROM TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antheraea polyphemus (Polyphemus moth).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysla;
Bombycoidea; Saturniidae; Saturniinae; Antheraea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1988 (Rel. 09, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CHORION CLASS CB PROTEIN PC404 (FRAGMENT).
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                                                                                                                                                                                                                                     EMBL; J01160; AAA27787.1; -.
EMBL; V00079; CAA23421.1; ALT_TERM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=83195030; PubMed=6573656;
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SIMILARITY: MEMBER OF THE BETA-BRANCH OF CHORION PROTEIN TO WHICH
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Pred. No.
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31;
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p47798; Q28025;
01-FEB-1996 (Rel. 33, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (MELANOTROPIN RECEPTOR) (MC1-R) (BDF3).
MC1R OR MSHR.
MC1R OR MSHR.
                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE~94307438; PubMed~8034052;

Vanetti M., Schoenrock C., Meyerhof W., Hoellt V.;

"Molecular cloning of a bovine MSH receptor which is highly expressed "molecular cloning of a bovine MSH receptor which is highly expressed in the testis.";
                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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Klungland H., Roed K.H., Vage D.I.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mamm.
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MEDLINE-96325106; PubMed-8661706;

Joerg H., Fries H.R., Meijerink E., Stranzinger G.F.;

Joerg Coat Coat Color in Holstein cattle is associated with a deletion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
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                                                                                S71017; AAB31361.1;
U39469; AAC48590.2;
Y13957; CAA74291.1;
Y19103; CAB64818.1;
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PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR00536; MELNOCYTESHR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G_PROTEIN_COUPLed receptor; Transmembrane;
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Search completed: September 28, 2001, 12:39:12 Job time: 787 sec

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|1263 TEVGAIATDT 1272
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"Phylogenetic analysis of members of the genus Rickettsia using the gene coding the outer-membrane protein rOmpB (ompB).";

Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).

EMBL; AF123718; AAF34121.1; -.

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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettslaceae; Rickettsleae; Rickettsia.
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation updat
HYPOTHETICAL 57.0 KDA PROTEIN.
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF211820; AAG43541.1; -.
SEQUENCE 1643 AA; 169818 MW; 68FFBBCE87E496B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Phylogenetic analysis of the romp B genes of Rickettsia Rickettsia prowazekii European human and North American squirrel strains.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF211821; AAG43542.1; -.
SEQUENCE 1643 AA; 169767 MW; D22EF05D9DB01AAE CRC64;
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Moron C.G., Bouyer D.H., Yu X.-J., Foil L.D.,
Walker D.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rickettsiaceae;
NCBI_TaxID:782;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
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Pred. No. 0.72
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48; DB 2
Pred. No. 0.72;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1643
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ي.72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Crocquet-Valdes P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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Q9KKA9
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AC Q9
DT 01
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Best Local
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              Q9KKA9
Q9KKA9;
01-OCT-2000
01-OCT-2000
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SEQUENCE 52
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253 TFIGAIPTET
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RX KEDLLINE-98044033; PubMed-9384377;
RX KEDLINE-98044033; PubMed-9384377;
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borniss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borniss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Brotiss R., Boursier K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Giseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Kurita K., Lavine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Mosestl D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Schouska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Rieger M., Tamakoshi A., Tanaka T., Tarahashi H., Takamaru K.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Ra Kuritas P., Wipat A., Yamanoto H., Yamane K., Yasumoto K., Yata K.,
RA Winters P., Wipat A., Yamanoto H., Yamane K., Yasumoto K., Yata K.,
The complete genome sequence of the gram-positive bacterium Bacillus
The Subtliks ",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kunst F., Ógasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ data
EMBL; 294043; CABO8050.1; -.
EMBL; 299121; CAB18452.1; -.
Interpro; IPR001899; -.
Interpro; IPR002027; -.
Interpro; IPR002293; -.
Interpro; IPR002293; -.
Pfam; PF00324; aa_permeases; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium Bacillus/Staphylococcus group; Bacillus.
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                                                                                                                                                                                                                                                                                                                             1 TFIGAIATDT 10
                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
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520 AA; 5
(TrEMBLrel. 15, (TrEMBLrel. 15,
                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56988 MW;
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Created)
Last sequence update)
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Pred. No. 8.
                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                     1616
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
8.2;
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RESULT RESULT DYXC45 PAC Q9 PA
RESULT
Q9KKB2
ID Q9
AC Q9
DT 01
DT 01
DT 01
DT 01
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 7
                             Q9KKB2;
Q9KKB2;
01-OCT-2000
01-OCT-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN-MALISH 7;

Stenos J., Walker D.;

Stenos J., Walker D.;

The rickettsial outer membrane protein A and B genes of Rickettsia australis, the most divergent rickettsia of the spotted fever group.";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF149110; AAD39533.1;

InterPro; IPR001639; -.

PRINTS; PR00810; BCTERTALGSPC.

NON_TER
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Q9XC45;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
OUTER MEMBRANE PROTEIN B (FRAGMENT).
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=45261;
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PubMed=10939649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
Rickettsiaceae; Rickettsie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rickettsia conorii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=781;
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                                                                                                                                                                                                                                                                                                                                                               951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TFIGAIATDT 10 : | : | : | | | | | |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 77.77; Conservative
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                             (TrEMBLrel.
                                                              (TrEMBLrel.
                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                               959
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70
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77
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16,
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                                     Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; Pred. No.
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                                     update)
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NON_TER
SEQUENCE
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
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"Phylogenetic analysis of members of the genus Rickettsia gene coding the outer-membrane protein rOmpB (ompB).";

Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).

EMBL; AF123708; AAF34111.1; -.

NON_TER 1614 1614
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsiae; Rickettsia.
                                                                         OMPB.
                                                                                                OMPB (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Astrakhan rickettsia.
Bacteria, Proteobacte
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      Bacteria;
                                       Rickettsia sp.
                                                                                                                                                                                                                                                                Q9KKA4
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NCBI_TaxID=140892;
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   Proteobacteria; alpha
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77.88;
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         subdivision; Rickettsiales;
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Mismatches
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Raoult D.;
Ra new SFG rickettsia i
Ra new SFG rickettsia i
Ra new SFG rickettsia i
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01-OCT-2000
01-MAR-2001
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STRAIN STRAIN S;
PubMed-10939649;
PubMed-10939649;
ROUX V. Raoult D.;
"Phylogenetic analysis of members of the genus Rickettsia using gene coding the outer-membrane protein rOmpB (ompB).";
Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
EMBL; AR13720; AAF34123.1; -.
NON_TER 1615 1615
SEQUENCE 1615 AA; 164362 MW; 239387B0B84E267B CRC64;
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SEQUENCE
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Bacteria; Proteobacteria; alp
Rickettsiaceae; Rickettsieae;
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NCBI_TaxID=45263;
                                                                                                                                                                                                                                   Q9KKB8
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ROUX V., RBOULT D.;
Submitted (DEC-1999) to the
EMBL; AF210695; AAG48556.1;
                                                                           OMPB (FRAGMENT).
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                      Rickettsia
                                                     OMPB
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77.8%;
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77.88;
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to the EMBL/GenBank/DDB
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alpha
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(FRAGMENT).
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01-MAR-2001 (TrEMBLrel. 1
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Q1-QCT-2000 (TrEMBLrel. 15,
Q1-QCT-2000 (TrEMBLrel. 15,
Q1-MAR-2001 (TrEMBLrel. 16,
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"Phylogenetic analysis of members of the genus Rickettsia using the gene coding the outer-membrane protein rOmpB (ompB).";

Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).

EMBL; AF123706; AAF34109.1; -.

NON TER 1616 1616

SEQUENCE 1616 AA; 164248 MW; E4B06C912859D5A6 CRC64;
Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsieae; Rickettsia. NCBI_TaxID=35791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROUX V., Raoult D.;

ROUX V., Raoult D.;

ROUX V., Raoult D.;

ROUX V., Raoult D.;

Phylogenetic analysis of members of the genus Rickettsia using gene coding the outer membrane protein rOmpB (ompB).";

Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).

EMBL; AF123711; AAF34114.1; -.

NON_TER 1616 1616

1616 AA; 164500 MW; 8053C358A44A72D9 CRC64;
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                                                                          Rickettsia massiliae.
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Rickettsiaceae; Rickettsieae;
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eae; Rickettsia.
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Q1-MAR-2001 (TremBLrel. 16,
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O1-OCT-2000 (TremBLrel. 15,

O1-OCT-2000 (TremBLrel. 16,
                                       Rickettsia rhipicephali.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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STRALN-MACULATUM 20;
PubMed-10939649;
Roux V. Raoult D.;
Phylogenetic analysis of members of the genus Rickettsia using gene coding the outer-membrane protein rompB (ompB).";
Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
EMBL; AF123717; AAF24120.1; -.
NON_TER 1616 1616
SEQUENCE 1616 AA; 164254 MW; 3D270DF9D5C16208 CRC64;
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"Phylogenetic analysis of members of the genus Rickettsia using the gene coding the outer-membrane protein rOmpB (ompB).";
Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
EMBL; AF123714; AAF34117.1; -.
NON_TER 1616 1616
SEQUENCE 1616 AA; 162964 MW; 9CF6EA2BAlB7821D CRC64;
SEQUENCE FROM N.A. STRAIN-3-7-6;
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PubMed-10939649;
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RROUX V., Raoult D.;
RPOY V., Raoult D.;
Phylogenetic analysis of members of the genus Rickettsia using the gene coding the outer-membrane protein rOmpB (ompB).";
Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
EMBL; AF123719; AAF34122.1; -.
NON_TER 1616 1616
SEQUENCE 1616 AA; 163270 MW; 42E0489239F15EB4 CRC64;
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September 28, 2001, 10:00:15; Search time 1261.48 Seconds (without alignments) 367.848 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

8	7	6	თ	4	ω	2	1	Result No.
23	28.4	28.4	28.4	28.4	28.4	28.4	30	Score
76.7	94.7	94.7	94.7	94.7	94.7	94.7	100.0	Query Match Length DB
2794	5319	5131	5015	5015	5015	4851	5258	Length
7	9	w	N	N	N	<b>ب</b>	ω	DB BDB
AF284000	AR019483	RIRSPAP	AF211821	AF211820	AF161079	AF123718	RIRCSLPT	ID
AF284000 Chaetophr	AR019483 Sequence	M37647 Rickettsia	AF211821 Rickettsi	AF211820 Rickettsi	AF161079 Rickettsi	AF123718 Rickettsi	L04661 Rickettsia	Description

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SOURCE
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Rickettsia typhi.

Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Backettsiaceae; Rickettsieae; Rickettsia; typhus group.

1 (bases 1 to 5258)
Hahn,M.J., Kim,K.K., Kim,I. and Chang,W.H.

Cloning and sequence analysis of the gene encoding the crystalline surface layer protein of Rickettsia typhi

Gene 133 (1), 129-133 (1993)
                                                                                                                                                                    Gene 133
94040787
                                                                                                                                                                                                                                                                                                                                   gene, complete cds.
                                                                                                                                                                                                                                                                                                                                             RIRCSLPT 5258 bp DNA BCT 10-MAR-Rickettsia typhi crystalline surface layer protein (slpT)
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/transl_table⊹11
                         /gene¬"slpT"
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                                                                                        /db_xref~"taxon:785"
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                                                                                                                            organismo"Rickettsia typhi"
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AF273674 Plasmodiu
AF210695 Rickettsi
AF123707 Rickettsi
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Direct Submission
Submitted (27-JAN-1999) Unite des Rickettsies, Faculte
27 Boulevard Jean Moulin, Marseille 13385, France
                                                                                                                                                                                                                                                                                                                                                                           Roux. V. and Raoult.D.

Phylogenetic analysis of members of the genus Rickettsia using the gene encoding the outer-membrane protein rOmpB int. J. Syst. Evol. Microbiol. 50 Pt 4, 1449-1455 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rickettsia prowazekii
Rickettsia provazekii
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
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Roux, V. and Raoult, D.
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Location/Qualifiers
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aaattvdgagfdgtgagvnlpvatnsvitansnnaitfntpngnlnslfldtantlav
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/protein_id="AAB48987.1"
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/organism="Rickettsia prowazekii"
/strain="Breinl"
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Direct Submission
Submitted (21-JUN-1999) Pathology, University of Texas Medical
Branch, 301 University Blvd., Galveston, TX 77555-0609, USA
                                                                                                                                                                                                                                       Rickettsia prowazekii
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettslaceae; Rickettsleae; Rickettsia; typhus group.
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                                                                                    2 (bases 1 to 5015)
Moron, C.G., Yu, X.J.
                                                                                                                                                                                        1 (bases 1 to 5015)
Moron, C.G., Yu, X.J. and Walker, D.H.
                                                                                                                                                                                                                                                                                                                                                                                              complete cds.
AF161079
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                                                                                                                                                                Sequence analysis of ompB
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GTTTIK QDNANANFSCTQAYTLIQGGARFNGTLGAPNFAYTGSINIFVKYELIRDSNA
DYVLTRTNDVLUNVTTAVGNSAIANAFGVSQNISCKESTNTAAYNNHLLAKDPSDVA
TFVGAIATDTSAAVTTNNLNDTQKTQDLLSNRLGTLRYLSNAETSDVAGSATGAYSSG
DEAEVSGYGVNAKFFYNIAEQDKKGGIAGYKAKTTGVVVGLDTLASDNLMIGAAIGITK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSIFKLADGTVINGPVNONALMNNNALAAGSIQLDGSAIITGDIGNGGVNAALQHITLANDASK LALDGANIIGANVGGAIHFQANGGTIKLTNIGNNIVVNFDLDITDKTGSVOANDASK LALDGANIIGAVGGAIHFQANGGTIKLTNIGNIVVNFDLDITDKTGSVODANGSKILNOFLITINGSVGTUANTKTLAQLNIGSSKTILNAGDVAINELVIENNGSVOLNHNIYLLTKTINAANGGQIIVAADPLNTNTTLADGTNLGSAENPLSTIHFATKAANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QTAPFISQPDRTAKTSYNIGLSANIKSDAKMEYGIGYDFNSASKYTAHQGT"
1713 c 922 g 1581 t
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GKMSKQIAAGNYDNMTFGGNLIFGYDYNAMPNVLVTPMAGLSYLKSSNENYKETGTTV
ANKRINSKFSDRVDLIVGAKVAGSTVNITDIVIYPEIHSFVVHKVNGKLSNSQSMLDG
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TYKFLGDTTFNGGTKIEGKSILQISNNYTTDHYESADNTGTLEFYNTDPITYTLNKQG
AYFGYLKQVIISGPGNIYFNEIGNYGIYHGIAANSISFENASLGTSLFLPSGTPLDVL
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VTINDDVTLTTGGIAGTDFDAKITLGSVNGNANVRFVDSTFSDPRSMIVATQANKGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIKSTYGNGTYDNFNAPIYYYSGIDSMINNGQIIGDKKNIIALSLGSDNSITYNANTL
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KNNGNTAGVITFNANGALVSASTDPNIAVTNINAIEAEGAGVVELSGIHIAELRLGNG
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KLISQGGAANAVIGTDNGAGRAAGFIVSVDNGNAATISGQVYAKNMVIQSANAGGQVT
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TGQGITVQEASNTINAQNALTKVHGGAAINANDLSGLGSITEAAAPSVLEENLINPTT
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/protein_id="AAF34121.1"
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                                                                                                                                                                                                                                                                                                                                                                         GI:5353762
                                                                                    Yu, X.J. and Walker, D.H.
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                                                                                                                                                                of Rickettsia
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LAAGSIQLDGSAIITGDIGNGGVNAALQHITLANDASKILALDGANIIGANVGGAIHF
QANGGTIKLTWYQNNIVVNFDLDITTDKTGVVDASSLINNQTLTINGSIGTVVAANTKT
QANGGTIKLTWYQNNIVVNFDLDITTDKTGVVDASSLINNQTLTINGSIGTVVAANTKT
QANGGTIKLTWYQNNIVVNFDLDITTDKTGVVDASSLINNQTLTINGSIGTVVAANTKT
QANGGTIKLTWYGNATUVNFDLDITTDKTGVVDASSLINNQTLTINGIITAVAANQGAIITA
LAQLAIIGSKRILAAGDVAIRELVIENNGSVOLNHNYYLITKTINAANQGAIITVAADP
LNTNITLADGTNLGSAENPLSTIHFATKAANADSILNVGKGVNLYANNITTNDANVGS
LHFRSGGTSIVSGTVGGQQGHKLNNLILDNGTTVKFLGDTFWAGGTKIEGKSILQISN
LHFRSGGTSIVSGTVGGQQGHKLNNLILDNGTTWKFLGGTWINAGTVDANVGSIDS
LHTRSGGTSIVSGTLEFVNTDPITYTLKKQGAYFGVLKQVIISGGGNIVFNETGNVG
IVHGIAANSISFENASLGTSLFLPSGTPLDVLTIKSTVGNGTVDNENAPIVVSGIDS
MINNGQIIGDKKNIIALSLGSDNSITYWANTLYSGIRTKNNQCTVTLSGGMPNNPGT
IYGLGLENGSPKLKQVTFTTDYNNLGSITANNVTINDDVLLTTGGILACTDFDAKITLG
SVNGNANVRFVDSTFSDPRSMIVATQANKGTVTYLGNALVSNIGSLDTPVASVRFTGN
DSGAGLOGNIYSQNIGFGTYNLTILNSNVILGGGSTAINGEIDLLTNNLIFANGTSTW
GDNTSISTTIAVSSGNIGQVVIAEDAQVNATTTGTTIKIQDNANANTSGTQAYTLIQ
GGARFNGTLGAPNFAVTGSNIFVKYELLRDSNQDYVLTRTNDVLNVVTTAVGNSAIAN
AAPGVSQNISRCLESTNTAAYNMLLAKDPSDVATFVQAIATDTSAAVTTVNLNDTQKT
GDLLSNRHENGTLAXVGSAATANALAKAGOASGATALGAAGNYDMAGSEGGNILFGY
SOOLVKNFFAQGNSIFTLNKVNSKSORYFFESNKKMSKQIAAAGNYDMAGFEGGNILFGY
SOOLVKNFFAQGNSIFTLNKVNSKSORYFFESNKKMSKQIAAAGNYDMAFFEGGNILFGY
SONLMANDAVITTBUAGTGTT SVI SCENENVETGTONGTNAGANGTNONTTTTOTT SVI
KSDAKMEYGIGYDFNSASKYTAHQGTLKVRVNF"
1 732 c 948 g 1638 t
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AAATTEDGIGEDQAAGANIPVAPNSVITANANDIATT
INEDTIGETUAAGAGNIPVAPNSVITANANDIETENTPNGHINLELDTANDLAVT
INEDTIGETUNIAQQAKERNETVAAGKILAITGGGTTVQEASNTINAQNALTKVNGG
AAINANDLSGLGSITFAAAPSVLEFNLINPTTQEAPLTLGANSKIVNGGNGTLNITNG
FIQVSDNTFAGIKTINIDDCQGLMFNSTPDAANTLNIDAGGNTINFNGIDGTGKLVLV
SKNGAATEFNVTGTLGGNLKGIIELNTAAVAGKLISQGGAANAVIGTDNGAGRAAGFI
VSVDNAATISGQVYKANMVIQSANAGGOVTEHIVDVGLGGTTNFKTADSKVIITE
NSNFGSTNFGNLDTQIVVPDTKILKGNFIGDVKNNGNTAGVITFNANGALVSASTDPN
                                                                                       DYNAMPNYLYTPMAGLSYLKSSNENYKETGTTYÄNKRINSKFSDRYDLIYGAKVAGST
YNITDIYIYPEIHSFYYHKYNGKLSNSQSMLDGQTAPFISQPDRTAKTSYNIGLSANI
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/protein_id="AAD42234.1"
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/strain="Breinl"
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ORIGIN BASE COUNT

Š Matches Query Match Best Local Similarity l acatttataggagctattgctacagataca 30 29; Conservative 94.78; 96.78; 0; Mismatches Score 28.4; Pred. No. 0. .14; B 2 Length 5015; Indels 0 Gaps

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3969 ACATTTGTAGGAGCTATTGCTACAGATACA 3998

REFERENCE AUTHORS VERSION KEYWORDS RESULT AF211820 SOURCE ACCESSION DEFINITION Locus TITLE ORGANISM Rickettsia prowazekii.
Rickettsia prowazekii.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia; typhus group.
1 (bases 1 to 5015)
1 (bases 1, Bouyer, D. H., Yu, X.-J., Foil, L. D., Crocquet-Vald Phylogenetic analysis of the romp B genes of Rickettsia felis and Rickettsia prowazekii European human and North American flying and Walker, D.H. AF211820.1 Rickettsia prowazekii strain Florida outer membrane protein (ompB) gene, complete cds. AF211820 AF211820 Bouyer, D.H., Yu, X.-J., GI:12003367 5015 bp DNA Foil, L.D., Crocquet-Valdes, P. 02-JAN-2001 ne protein B

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JOURNAL
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AF211821
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  Rickettsia
Rickettsia
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AF211821.1
                                                                                                                                                           AF211821 5015 bp DNA BCT 02-JAN-200:
Rickettsia prowazekii strain Virginia outer membrane protein
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Moron, C.G., Bouyer, D
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GGARFNGTLGADNFA VYGSNIFVKY ELLENDSNDDYTTT KIQDNANANESGTQAYTLIQ
GGARFNGTLGADNFA VYGSNIFVKY ELLENDSNDYAIRTDTSAAVTTVULNUTQKT
APVSQNI SRCLESTNTAAYNNMLLAKDPSDVATFVGAITDTSAAVTTVULNUTQKT
QDLLSNRLGTLRY LSNAETSDVAGSATGAVSSGDEAEVSYGVWAKPFYNIAEQDKKGG
IAGYKAKTTGVVVGLDTLASDNLMIGAAIGITKTDIKHQDYKKGDKTDINGLSFSLYG
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LNTNTTLADGTNLGSAENPLST I FFATKAANADS ILNVKKGVNLYANNITTNDANVGS
LHFRSGGTS I VSGTVGGOGGIKLNNLLILDNGTTVKFLGDTTFNGGTK IEGKSILQISN
NYTTDHVESADNTGTLEFVNTDP ITVTLNKQGAYFGVLOVI ISGFGNIVFNEIGNVG
I VHG LAANS I SFENASLGT SLE FLPSGTP LDVLT IKSTVGNGTVNEPNAP I VVVSG IDS
MINKOQI IGOKKNI I ALSLGSDNS ITVNANTLY SGI FPTKNNOGTVTLSGGMENNFGT
I YGLGLENGSPKLKQVTFTTDY NNLGSI I ANNVT I NDDVTLTTGG I AGTDEDAKITLG
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VSUDNGNAATISGQVYAKNNYIQSANAGGQVTFEHIVDVGLGGTUNFKTADSKVIITE
VSUDNGNAATISGQVYDTKIIKGNEIGDVTFEHIVDVGLGGTUNFKTADSKVIITE
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IAVTNINAIEAEGAGVVELSGIHIAELRLGNGGSIFKLADGTVINGPWQNALMNNNA
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QANGGTIKLTNTQNNIVVNFDLDITTDKTGVVDASKILNQTLTINGSIGTVVANTKT
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731 c 950 g 1637 t
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DSGAGLQGNIYSQNIDFGTYNLTILNSNVILGGGTTAINGEIDLLTNNLIFANGTSTW
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INEDTTLGFITNIAQQAKFFNFTVAAGKILNITGQGITVQEASNTINAQNALTKVHGG
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/protein_id="AAG43541.1"
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/strain⇔"Florida"
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/transl_table=11
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prowazekii.
prowazekii
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                                                                                    GI:12003369
                                                                                                                                       complete cds.
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Pred. No. 0.
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Mismatches

Similarity

94.78;

Score 28.4; DB Pred. No. 0.14;

DB 2;

Length 5015;

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Query Match Best Local

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1 (bases 1 to 5015)
Moron, C.G., Bouyer, D.H., Yu, X.-J., Foil, L.D., Crocquet-Vald
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Direct Submission
Submitted (06-DEC-1999) Pathology, University of Texas Medical
Branch at Galveston, 300 University Blvd., Galveston, TX 77555, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phylogenetic analysis of the romp B genes of Rickettsia felis and Rickettsia prowazekii European human and North American flying
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LAQLNIGSSKTILNAGDYA INELVIENNGQVQLNHNTYLITKTI NAANGQII VAADP
LATUTILAGETHLGASAEN INELVIENNGQVQLNHNTYLITKTI NAANGQII VAADP
LNTUTILAGETHLGASAENDLSTIHAFNKAANADSILLVGKGVULYANNITTNDANUGS
LHFRSGTSIVSGTVGGQQGHKLNNLILDNGTTVKFLGDTTFNGGTKIEGKSILQISN
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IVHGIAANSISEENASIGTSLEFVSGTPLDLVLPIKSTYGNGTVDNENAPIVVVSGIDS
NINNGQIIGDKKNIIALSGTSLEFVSGTPLDLVLPIKSTYGNGTVDNENAPIVVVSGIDS
MINNGQIIGDKKNIIALSGTSLEFVSTDVNNLGSITANNTINDDVTLTTGGIAGTDEDAAITLG
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DSGAGLIGGNIYSQNIDFGTYNLTILLSNVILGGGTTALNGEIDLLTNNLIFANGTSTW
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DSGAGLIGGNISSGNIGQVVILAEDAQVNATTTGTTTIK IQDNANAFSGTQAYTLA
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FIQVSDNTFAGIKTINIDDCQGLMFNSTPDAANTLNLQVGGNTINFNGIDGTGKLVLV
SKNGAATEFNVTGTLGGNLKGIIELNTAAVAGKLISQGGAANAVIGTDNGAGRAAGFI
                                                                                                       DYNAMPNYLYTPMAGLSYLKSSNENYKETGTTVANKRINSKFSDRVDLIVGAKVAGST
VNITDIVIYPEIHSFYVHKVNGKLSNSQSMLDGQTAPFISQPDRTAKTSYNIGLSANI
                                                                                                                                                                                                                       GGARENGTLGAPNFAVTGSNIFYKYELIRDSNQDYULTRTNDVLNVYTTAVGNSAIAN
APGYSQNISRCLESTNYAAYNNMLLAKDPSDVATFYGAIATDTSAAVTTYNLNDTQKT
QDLLSNRLGTLRYLSNAFTSDVAGSATGAVSSGDEARVSYGYVAKRFYNIAEDDKKGG
IAGYKAKTTGVVVGLDTLASDNLMIGAAIGITKTDIKHQDYKKGDKTDINGLSFSLYG
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NSNIKGSTNIKGNLDTQIVVPDTKILKGNFIGDVKNTAGVITFNANGALVSASTDPN
IAVIMINAILBAEGAGVVELKGCIHIABLIRLGNGGSIFKLADGTVINGPVRQNALMINNA
LAAGSIQLDGSAIITGDIGNGGVNAALOHITLANDASKILALDGANIIGANVGGAIHF
                                      KSDAKMEYGIGYDFNSASKYTAHQGTLKVRVNF"
735 c 951 g 1635 t
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/protein_id="AAG43542.1"
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/transl_table=11
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/strain="Virginia"
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BASE COUNT
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MEDLINE
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                                                                                                                                 Query Match
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  3995
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29; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-layer protein; surface antigen.
Rickettsia prowazekii (strain Brein 1) DNA.
Rickettsia prowazekii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rickettsia prowazekii surface protein antigen (spaP) gene, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
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TTGTTTIKIDNANANFSGTQAYTLIQGGARRNGTLGAPNFAYTGSNIFVKYELIRDS
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VATFYGAIATDTSAAVTTVNLINDTQKYQDLLSNRLGTLRYLSNAETSDVAGSATGAVS
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TKTDIKHQDYKKGBKTDINGLSFSLYGSQQLVKNFFAQGNSIFTLNKYKSKSQRYFFE
                                                                                                                                                                                                                                                                                                              TVANKRINSKESDRVDLIVGAKVAGSTVNITDIVIYPEIHSEVVHKVNGKLSNSQSML
DGQTAPFISQPDRTAKTSYNIGLSANIKSDAKMEYGIGYDFNSASKYTAHQGTLKVRV
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LANDASKILALDGANIIGANVGGAIRTGOANGGTIKLTWYQNNIVNFDLDITTDKTGV
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GAYFGVLKQVIISGPONIVFNEIGNVGIVHGIAANSISFENASLGTSLFLPSGTPLDV
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TFEHIVDVGLGGTTNFKTADSKVIITENSNFGSTNFGNLDTQIVVPDTKILKGNFIGD
VKNNGNTAGVITFNANGALVSASTDPNIAVTNINAIEAEGAGVVELSGIHIAELRLGN
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TGQGITVQEASNTINAQNALTKVHGGAAINANDLSGLGSITFAVCPSVLEFNLINPIN
SRSSSYHLVSNSKIVNGGNGILNITNGFIQVSDNTFAGIKTINIDDCQGLMFNSTPDA
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LYSGIRTTKNNQGTYTLSGGMPNNPGTIYGLGLENGSPKLKQVFTTTDYNNLGSIIAN
NYTINDDVTLJTGGIAGTDFDAKITLGSVNGHANVRFYDSTESDPRSHIYATQANKGT
TYYLGNALYSNIGSLDTPVASVRFTGNDSGAGLQGNIYSQNIDFGTYNLTILNSNVIL
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/protein_id="AAA26390.1"
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/strain="Brein 1"
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Sequence 1:
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Patent: US 5783441-A 1 21-JUL-1998;
Location/Qualifiers
1. .5319
                                                                                                                                                                                                                                      Submitted (30-JUN-2000) Biology, University of California, 1354 Spieth, Riverside, CA 92521, USA
                                                                                                                                                                                                                                                                               2 (bases 1 to 2794)
Madsen,O., Scally,M., Douady,C., Kao,D.,
Amrine,H., Stanhope,M., de Jong,W. and S
                                                                                                                                                                                                                                                                                                                                                                                 Madsen,O., Scally,M., Douady,C.J., Kao,D.J., DeBry,R.W., Adkinmrine,H.M., Stanhope,M.J., de Jong,W.W. and Springer,M.S. Parallel adaptive radiations in two major clades of placental
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chaetophractus villosus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF284000 2794 bp
Chaetophractus villosus
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Carl,M., Dobson,M.E., Ching,W. and Dasch,G.A.
Gene and protein applicable to the preparation
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/product-"BRCA1"
/protein_id-"AAK15587.1"
/protein_id-"AAK15587.1"
/db_xref-"GI:13195175"
/tanslation-"CGINTHANLLQHENSSLLLTKDRVNVEKAEFCNKSKQPGLARRQ
/translation-"CGINTHANLLQHENSSLLYGKKELNKQKLPCSESPROTQDIPWITL
NSSIQKVNEWFSRSDDLLTSDDSHDGGSESKAEVAGALKVPNEVNGYSSSSEKIDLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="unknown"
766 c 983 g
                                                                                                           /note="similar to
                                                                                                                                                                       organism="Chaetophractus villosus"
/db_xref="taxon:29080"
                                                                                              /codon_start=2
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Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (04-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestes clonerequest@sanger.ac.uk clonerequest@sanger.ac.uk on Jul 14, 2000 this sequence version replaced gi:8250069. During sequence assembly data is compared from overlapping clones.
                                                                                                                                                      http://www.sanger.ac.uk/HGP/Chrl
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP4-586015 is from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STSs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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This sequence is the entire insert of clone RP4-586015 The true
                                    VECTOR: pCYPAC2
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                                                            http://www.chori.org/bacpac/home.htm
                                                                                                                           the library RPCI-4 constructed by the group of Pieter de Jong. For
                                                                                                 urther details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1052
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SVSLLEADTLGKAKTALNQPMSQYAAIKATELSHGCAKDTRNDYH
TQETSVEMESSELDTOYLQNIFKISKROGSFALESNPENECATVCAHSRFLDKGSSFXV
FECRQKEENOGKKESKIKHVQAVHTTAGFPVVCQKDKPGDYAKCSIQEVSRLCQSSQF
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ANSGHENETKGDYVQKEENANPLESLEKESAFFRYGEBPISSSISKINELELNIYNSKAS
KKNRLRRMSSTRHIHALELVQNRNPSPPKHTELOIDSCGSTEEIEKINSMOKPIRHNR
MLQLMKEKENTTGAKKNNKPNEQISERHASDVFPELKLINVTDFLPKCSNPDKLQEFV
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Pred. No.
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.1 KDA protein, ESTs,
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VERSION KEYWORDS

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AUTHORS

JOURNAL TITLE

COMMENT

RESULT 9 AL139014/c

DEFINITION

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Matches

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="dJ586015.1"
9984. .1001=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence=not_experimental
/product="dJ586015.1 (hypothetical 22.1 KDA protein)"
/protein_id="CAC36064.1"
/db_xref="GI:13559035"
/translation="TDCTVFRIHTKAEGFMDADIPLELVFHLPVNYPSCLPGISINSE
/translation="TDCTVFRIHTKAEGFMDADIPLELVFHLPVNYPSCLPGISINSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
/product="dJ586015.1 (hypot6174. .9293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="match: cDNAs: Em:AL050062
match: ESTS: Em:AI035684 Em:AI591890 Em:AI162458
Em:AA177712 Em:AW227581 Em:AW269377 Em:AA115559
Em:AA336662 Em:AI344603 Em:AA825527 Em:,AI457123
Em:AA483584 Em:AI370117 Em:R19361 Em:N80756 Em:AI49762
Em:AI566566 Em:R07610 Em:AW6613686 Em:AA336253 Em:AA770533
Em:AI023354 Em:AA699431 Em:AI187083 Em:AA1969585"
                                                                                                                                                                 /note="LTR41 repeat: matches 90.
complement(12559. 13029)
/note="match: GSS: Em:AQ375128"
complement(12653. 13029)
/note="match: STS: Em:AF192021"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="dJ586015.1"
<6174. .6676
/gene="dJ586015.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match: STS: Em:HSPE32C12" 3609. .4115
                                                                                                                                                                                                                                                                                                                                                                   /note="16 copies 2 mer tt 84% conserved" complement(10605, .11104) /note="match: GSS: Em:AQ406955" complement(10624, .11071)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3609. .4115
/note="LTR22 repeat: matches 1. .580 of consensus"
/noin(<6174. .6678,8719. .9293)
                                                            /note="HERVL repeat: matches 3756.
14701. .14847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(8370.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(6407. .6852)
/note="match: STS: Em:HSPE52C06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKVPKS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STIMDDGLWITLLHLDHMRAKTKYVKIVEKWASDLRLIGRLMFMGKIILILLQGDRNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP4-586015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /map="p21.2-22.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/chromosome="1"
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                                                                                                       13606.
                                                                                                                                                                                                                                                                                                                        /note="match: GSS: Em:AQ123242"
11814. .11969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match: GSS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match: GSS: Em:AQ021020"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6849. .7492
/gene="dJ586015.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="dJ586015.1"
                                        /note="HERVL repeat: matches 3340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'organism="Homo sapiens"
                                                                                                                             note="HERVL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="dJ586015.1"
                                                                                                                                                  .13310
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                                                                                                                                                                                                                                                                                                    copies 39 mer 90% conserved"
                      5608
                                                                                                                         repeat: matches 4662.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .8651)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Em: AQ087817"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (hypothetical 22.1 KDA protein)"
                                                                                                                                                                                                                                                                . 159
.3340 of consensus
                                        .3476 of consensus"
                                                                                   .4662 of consensus
                                                                                                                                .5115 of consensus"
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                                          74262. .74289
700te="14 copies 2 mer ct 92% conserved" complement(75009. .75531)
700te="match: STS: Em:G56071
match: GSS: Em:AQ318565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="match: GSS: Em:AQ692409"
complement(64181. .64650)
/note="match: GSS: Em:AQ516612"
complement(64192. .64664)
/note="match: GSS: Em:AQ772035"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match: GSS: Em:AQ076357"
complement(49923, .50350)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="match: GSS: Em:AQ037084"
33228. .37447
/note="L1MA5A repeat: matches 2128. .6289 of consensus"
40468. .40909
                                                                                                                                                                          /note="32 copies 2 mer aa 67% conserved"
complement(73534. .73897)
                                                                                                                                                                                                                                                                                                      /note="match: GSS: Em:AQ308501" complement(68783. .69204)
                                                                                                                                                                                                                                                                                                                                                                                       /note="match: GSS: complement(64428. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="23 copies 2 mer tg 76% conserved"
complement(51169. .51637)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="match: GSS: complement(33002...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="21 copies 2 mer aa 83% conserved" complement(30902 .31318)
                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (64204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="match: GSS: Em:AQ798193"
complement(64146. .64653)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(62363. .62936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (60963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match: GSS: Em:AQ221216"
54190. .59443
fnote="LIPA2 repeat: matches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(31360. .31705)
/note="match: GSS: Em:AQ279514"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: GSS: Em:AQ229049"
complement(31360. .31705)
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23017. .23418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="HERVL repeat: matches 2343. .2665 of consensus" 19019. .19537
                                                                                                                                                                                                                                                              note="match: GSS: Em:AQ513641"
72119. .72225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="L1PA2 repeat: matches 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: GSS: Em:AQ115490" 50418. .50463
      'note="match: GSS: Em:AQ142531"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="match: GSS: Em:AQ395505"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match: GSS: Em:AQ007859"
31310. .31779
                                                                                                                                                        note="match: GSS: Em:AQ505770"
                                                                                                                                                                                                                                          'note="L1MA8 repeat: matches 6183.
                                                                                                                                                                                                                                                                                                                                                                        note="match: GSS: Em:AZ093975"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="LTR33 repeat: matches 5. .520 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="L1MA10 repeat: matches 6215. .6265 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="match: GSS: Em:AQ439345"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat: matches 1. .488 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                    .64657
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.33191)
                                                                                                                                                                                                                                                                                                                                                                                              64982
                                                                                                                                                                                                                                                                                                                                                                                                             Em: AQ165313"
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                                                                                                                                                                                                                                          .6288 of consensus"
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KEYWORDS
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: XGAP4; version 4.5 sequencing vector: plasm10; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 159742 bases at least Q40 consensus quality: 161714 bases at least Q30 consensus quality: 162661 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                               Insert size: 163347; sum-of-contigs
Insert size: 163310; 19.2% error; agarose-fp
Quality coverage: 4.32x in Q20 bases; sum-of-contigs Quality
coverage: 4.70x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: bA57H12
----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (20-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestes clonerequest@sanger.ac.uk
On Jul 15, 2000 this sequence version replaced gi:8217620.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG 20-JAN-2001 Homo sapiens chromosome 1 clone RP11-57H12 map p21.3-22.3, ** SEQUENCING IN PROGRESS ***, 10 unordered pieces. AL158082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 164247)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Caps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                     as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----- Project Information
        32594 32593: gap of 100 bp
32694 53020: contig of 20327 bp in length
53021 53120: gap of 100 bp
53121 94385: contig of 41265 bp in length
94386 94485: ~~~~
                                                                                                   1 25166: contig of 25166 bp in length
25167 25266: gap of 100 bp
25267 32593: contig of 7327 bp in length
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/note="match: GSS: Em:AQ895502"
complement(89454. .89956)
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81912. 81993
/note="41 copies 2 mer tt 67% conserved"
82463. 82777
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Pred. No. 80;
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RESULT 1
AL356152
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Homo sapiens chromosome 1 clone RP PROGRESS ***, 26 unordered pieces. AL356152 4 GI:9926611 HTGS_PHASE1; HTGS_DRAFT.
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24; Conser
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53121. .9
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/noten assembly_fragment:00788
fragment_chain:1"
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vector_side:right"
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fragment_chain:2
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fragment_chain:2"
151798. .164247
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fragment_chain:1"
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/chromosomea"1"
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fragment_chain:2"
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fragment_chain:2"
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fragment_chain:1"
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26066: gap of 100 bp
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Pred. No. 8
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                                                                                                                         clone RP11-335D10,
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Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 153468 bases at least Q40
Consensus quality: 163406 bases at least Q30
Consensus quality: 166479 bases at least Q20
Insert size: 169213; sum-of-contigs
Insert size: 189386; 6.1% error; agarose-fp
Quality coverage: 3.30x in Q20 bases; sum-of-contigs Quality
Coverage: 3.10x in Q20 bases; agarose-fp
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1 (bases 1 to 171713)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  20703 20802: gap of 100 bp 20803 29599: contig of 8797 bp in length 20803 29599: gap of 100 bp 29700 33636: contig of 6462 bp in length 33637 30736: gap of 100 bp 33737 40198: contig of 6462 bp in length 40199 40298: gap of 100 bp 40299 43998: contig of 3700 bp in length 43999 44098: gap of 100 bp 46584: contig of 2486 bp in length 46585 46684: gap of 100 bp 46585 46681: gap of 100 bp 40918 4917: contig of 2233 bp in length 49018 66152: contig of 2233 bp in length 66153 66252: gap of 100 bp 66253 78474: contig of 17135 bp in length 66253 78474: contig of 17135 bp in length 68253 78474: contig of 18222 bp in length 8340 83539: gap of 100 bp 92939: contig of 4865 bp in length 92940 93039: gap of 100 bp 92940 93039: gap of 100 bp 92940 93039: gap of 100 bp 93040 96452: contig of 3413 bp in length 96453 96552: gap of 100 bp 93040 96452: contig of 3413 bp in length 96453 96552: gap of 100 bp 93040 96452: contig of 3413 bp in length 96453 96552: gap of 100 bp
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16150 20702: contig of 4553 bp in length
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169380 171713: contig of 2334 bp in length
Location/Qualifiers
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/note="assembly_fragment:00273
fragment_chain:3"
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105973. .108830
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fragment_chain:2"
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155611: contig of 23973 l
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131538: cont
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127137: cont
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Dasypus novemcinctus BRCA1
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Spieth, Riverside, CA 92521, USA
Location/Qualifiers
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Maddsen,O., Scally,M., Douady,C., Kao,D., DeBry,R., Adkins,R.,
Amrine,H., Stanhope,M., de Jong,W. and Springer,M.
Direct Submission
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Mammalia; Eutheria; Edentata; Dasypodidae; Dasypus.
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                                                                                                                                                                                                                                                                                                                                         Submitted (19 NOV-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 23, 2000 this sequence version replaced gi:11225767.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                    The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RP11-810I22 is from the library RPCI-11.3 constructed at the
                                                                                                                                                                                                                                                                                                                  eature key.
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LQGEVAENLETIQVSDSTRDPEDLVVSGEKCLQTERSAESTGISVVPDTDYGTQDSIS
LLEADTLGKAKTALIQHVSQYVAIRNATELSHGCSKDTRUDTEDFKDSLRHEVNHTQG
TINVEIEESELDTQYLQNTFKISKRQSFALFSNEDNECATVCAHSRFLGKQFKVTFEC
RHKEENOGKKESKIKHVQVIHTTAGFPIVCQKDKPGDYAKGSIQGVSRLCQSSQARGN
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QSRWAESKETCNDRQTPSIEKKVDVDADPLYGRKELNKQKPPCSESHRDTQDIPWIML
NSSIQKVNEWFSRGDDILTSDDSHDRGSELNAEVAGALKVSKEVDEYSSFSEKIDLMA
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IQSTVSTISHSNIRENTFKEASSSSINEVGSSDENIQAEVGRNRAPKLNAMLRLGLMQ
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ITQEBSLQNKIKKRRTASGLAPEDLSKKVDLTVVGKTPEKINGGTDQMSQNDPVMNI
ANGGHENETMGDCVQKEKNANPTESLGKESAPRTKGEBISSSISMELELNILNSKAS
KKNRPKRMSSTRHIHALELVGSRNPSPPNHTELQIDSCSSIEEIEKINSNQKPIRHNR
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95.7%;
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Pred. No. let
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roswell Park Cancer Institute by the group of Pieter de further details see http://bacpac.med.buffalo.edu/
VECTOR: pBACe3.6
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                                                                                                                                                                                                                                                                                                                                                                   /note="Lmr-
9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MLT1F repeat: matches 177. .338 of consensus" 7548. .7863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="AluSq repeat: matches 1. .302 of 7092. .7226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MIR repeat: matches 132.
complement(5879. .6511)
/note="match: GSS: Em:AQ389784"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match: GSS: Em:AQ079663" 4833. .5299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 109.
4801. .5192
                                                                         complement(14581.
                                                                                                                                                                                                                                                                                                                                                                   8898.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MIR repeat: matches 14..153 of consensus" 7391..7547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(4436. .4748)
/note="match: GSS: Em:AQ111995"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="34 copies 2 mer ta 72% conserved" 1917. .2342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(1.
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/clone_lib="RPCI-11.3"
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complement(4436. .4748)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3426. .3872
/note="MSTB repeat: matches 3. .426 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3286. .3425
/note="MLT1D repeat: matches 363. .505 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="17 copies 4 mer atat 72% conserved"
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/db_xref="taxon:9606"
                                                                                                                                                              13855
                                                                                                                                                                                                                 /note="MIR repeat: matches 94. .252 of consensus"
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/note="62 copies 2 mer gt 79% conserved"
14670. .14785
                                                                                                 /note="L1PA8 repeat: matches 5949.
                                                                                                                                                                                                                                                             note="AluSx repeat: matches 1. .299 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MLT1F repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="AluSp repeat: matches 1. .313 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match: GSS: Em:AQ307374"
                                      note="match: 4662. .14785
                                                                                                                                       note="FAM repeat: matches 1. .168"
                                                                                                                                                                               'note="L1MA7
                                                                                                                                                                                                                                                                                                                                             'note="LTR39 repeat: matches 1.
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                                                                                                                                                      .14017
                                                                                                                                                                                                                                                                                                                                                                                   LTR18B repeat: matches 2. .592 of consensus"
                                                                                                                                                                                                                                            11038
                                                                                                                                                                               repeat: matches 5954.
                                                                                                                                                                                                                                                                                                     repeat: matches 1.
                                                           GSS: Em:AQ482234"
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                                                                                                                                                                                                                                                                                                                                                .794 of consensus*
                                                                                                                                                                                                                                                                                                     .214 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                              .177 of consensus"
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                                                                                                 .6160 of consensus
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                   /note="L1M4c repeat: matches 1. .1083 of consensus" 36464. .36679
                                                                                                                        33913. .34210
/note="AluSq repeat: matches 1. .297 of consensus"
                                                                                                                                                                                                                                                                      32631. .32799
/note="TAR1 repeat: matches 12. .157 of consensus"
33044. .33355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MER53 repeat: matches 108. .189 of consensus"
28555. .28702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="LTR40b repeat: matches 21..460 of consensus" 21996..22711 /note="LIMC5 repeat: matches 6671..7412 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="29 copies 4 mer gtgt 81% conserved"
complement(14691. 15151)
/note="match: GSS: Em:AQ393734"
14915. 16092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="L1MC3 repeat: matches 6660.
19218. .19552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"L1MC3 1
17710. .18073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="LTR17 repeat: matches 1..780 of consensus"
24632..25014
/note="HERVL32 repeat: matches 1537..1934 of consensus"
25492..25790
/note="AluSg repeat: matches 1..310 of consensus"
26219..26762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="LIMC/D repeat: matches 5434. .5464 of conser
20181. .20570
'note="MLTTIB repeat: matches 1. .390 of consensus"
20571. .20582
'note="LIMC/D repeat: matches 5467. .5601 of conser
21548. .21976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22795. .23848
"Note="HERVL32 repeat: matches 1934. .2914 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="MER5A repeat: matches 4. .186 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="LIM4 repeat: matches 3081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note "THEIC repeat: matches 1. .371 of consensus"
                                                                                                                                                                                                                                                                                                                                                       te="LTR9 repeat: matches 8. .560 of consensus"
69. .30570
69. LTR35 repeat: matches 63. .616 of consensus"
98. .32448
te="LIMA8 repeat: matches 5020. .6185 of consens:
25. .32806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e-"AluY repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e="MER53 repeat: matches 123. .177 of consensus"
3. .28174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e="L1ME repeat: matches 5263. .5576 of consensus"
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                                                                                                                                                                 e="MER50 repeat: matches 1. .49 of consensus"
9. .33708
e="L1MA8 repeat: matches 6183. .6286 of consenue"
                                                                                                                                                                                                                               e="AluSc repeat: matches 1.
2. .33608
                                                                                                                                                                                                                                                                                                                                      e="match: GSS: Em:AQ527057"
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repeat: matches 1257. .1500 of consensus"
                                                                                                                                                                 repeat: matches 6183. .6286 of consensus"
                                                                                matches 1953.
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                                                                                              Submitted (08-NOV-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Sep 15, 2000 this sequence version replaced g1:9838234.
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Submitted (12-JAN-2000) Genome
University School of Medicine,
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Waterston, R.H.
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Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
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Center project name: H_NH0496J03
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/note="Alux repeat: matches 3. .301 of consensus"
36979. 37428
/note="LLM4c repeat: matches 1500. .1887 of consensus"
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 511-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence H_NH0496J03 from base positions 144552 to 144902 is represented by sequence derived from PCR of clone DNA. Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The clone sequenced to the left is RP11-810122. this clone is at base position 1 of RP11-496J3; base position 220216 of RP11-496J3.
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10634.
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/db_xref⇔"taxon:9606"
/chromosome⇒"6"
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/clone_lib="RPCI-11"
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/rpt_family~"Alu"
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31132. .31518
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13039. .13095
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12341. .12591
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Dugong dugon
Eukaryota; Me
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Spieth, Riverside, CA 92521, USA
Location/Qualifiers
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2 (bases 1 to 2773)
Madsen,O., Scally,M., Douady,C., Kao,D., DeBry,R., Adkins,R., Amrine,H., Stanhope,M., de Jong,W. and Springer,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Sirenia; Dugongidae; Dugong.

1 (bases 1 to 2773)
Madsen,O., Scally,M., Douady,C.J., Kao,D.J., DeBry,R.W., Adkins,R., Amrine,H.M., Stanhope,M.J., de Jong,W.W. and Springer,M.S.
Parallel adaptive radiations in two major clades of placental
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LRRKSSTRHIHALELVUNNUSPPTHTELQIDSWSSSEEIKKSSEOKPVRHNRNLQLM
KNQETTTGAKKSKNFKEOLEKHASDAY PELMITSTICLITNCSSSHMYQEFNPSLQG
EEIEBMLGTIQVSNRTRDPEDLVLNGGRGLQTEISVESTS ISVIPDTDYSQNSISLI
EADTLRKAKTAPNQCASQCAA ENPNELIHGCPKDTRNDTEDFKDLLKCEVNHIQETC
VEMEDXELDTQYLQSTFKVSKQSFALFSNPEKECATICAHSKSLRKQSFKVTPEYGE
EEENQGNKESK KNEPKEQAVHTTAGY PEDCAFTYKSSIKGVSRLCQSSQFRGSE
SQHITACEHGISQNPDAMPLLSPIRASVKSKKNLSEERFEHTISLERAVKQNESIVQS
TVSTVSQNDIKESAKEASSSINEVGSSGENIRAELGRNRGFKLNAVLRLGLMQPEY
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/db_xref="taxon:29137"
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Query Match 69.3%; Score 20.8; DB 7; Length 2773; Best Local Similarity 91.7%; Pred. No. 1.8e+02; Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps Qy 3 atttataggagctattgctacaga 26
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Search completed: September 28, 2001, 11:17:52 Job time: 4657 sec

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AAX13139
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                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1460202
          Human secreted pro
cDNA encoding rp40
Methanococcus Jann
Human hydrolase-1i
Potato alpha-amyla
Alpha-amylase 1 pr
Human hTAFII105 cb
Transcription fact
                                                                                                                                                                                                    Description
                                                                                                                                                   Enterococcus faeca
                                                                                                                                                                    prowazekii S-la
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cDNA encoding TIAR	AAQ34556	14	1401	٠	17.8	45	ი
Arabidopsis thalia		21	1260	59.3	17.8	44	
Treponema pallidum	AAZ33112	20	585	•	17.8	43	ი
5 Complete	AAZ01425	20	1038602	60.0	18	42	
Human	⋗	21	6309	٠	18	41	ი
	AAA97552	21	5817	•	18	40	
Human	AAA97551	21	5817	60.0	18	39	
Rat sodium channel	AAC9060	22	3108	60.0	18	38	
Rat	AAC90602	22	2632	60.0	. 18	37	
	AAC67836	21	2220	60.0	18	36	
	AAX99605	20	1550	•	18	35	O
	AAC90601	22	645	60.0	18	υ 4	
	AAV52215	19	16995	60.7	18.2	33	
	AAV74675	18	10813		18.2	32	
	AAZ51236	21	9326	60.7	18.2	31	
Nucleic aci	AAX99656	20	1785	•	18.2	30	ი
	AAF27611	22	1167	•	18.2	29	
3	AAF27586	22	1167	60.7	18.2	28	
Sta	AAZ51239	21	1044	•	18.2	27	
	AAA71589	21	951	•	18.2	26	
Human colon car	AAC98552	21	580	60.7	18.2	25	
Staphylococcus aur	AAV78225	18	400		18.2	24	o
Staphylococcus aur	AAV78513	18	380	•	18.2	23	O
Staphylococcus aur	AAV79380	18	52		18.2	22	o
m	AAX13082	20	986	٠	18.4	21	
	AAV74652	18	4557	•	18.4	20	
~	AAV74732	18	2710	•	18.4	19	ဂ
Human gene signatu	$\vdash$	16	73	61.3		18	ი
Cosmid CVO14 conta	2	21	44576			17	ი
Cosmid CVO14 conta	N	21	44576	62.0		16	
Enterococcus faeca	AAX13213	20	20633	٠	•	15	
TANGO 275	825	22	4225	62.7		14	a
Human TANGO 275 op	AAF28253	22	3867	62.7		13	ი
Human latent trans	AAZ51929	21	3771	62.7	18.8	12	a

## ALIGNMENTS

R. prowazekii S-layer protein genomic DNA

28-SEP-1998 (first entry)

AAV35235

AAV35235 standard; DNA; 5319

ΒP

ب

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Key
-35_signal
                                             stem_loop
                                                                                                                   Rickettsia prowazekii.
                                                                                                                              Surface layer protein; S-layer; vaccine; typhus; spotted fever; infection; diagnosis; disease; ds.
      20-DEC-1993;
                 21-JUL-1998
                             US5783441-A
                                                                                     -10_signal
      93US-0169927
                                                        /*tag=__c
391..5229
/*tag=__d
                                                                         /*tag= a
363.368
/*tag= b
379.386
                                             /product s-layer protein 5270..5306
                                                                                                  340..345
                                                                                                       Location/Qualifiers
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RESULT 2
AAXI3139/c
ID AAXI311
XX AAXI31
XX AAXI31
XX IS Entero
XX Entero
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XX Entero
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AX Hol
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06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R. prowazekii strain Breinl. This sequence is useful for vaccination against typhus and spotted fever rickettsial infection or for diagnosing diseases caused by these bacteria. The surface layer protein antigens can be produced recombinantly in large quantities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-DEC-1993;
09-AUG-1991;
                                                        Claim 1; Page
                                                                                                                       New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and four raccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                WPI; 1999-045171/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX13139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4183 acatttgtaggagctattgctacagataca 4212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Column 11-24; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant DNA encoding Rickettsia surface for diagnosing typhus and spotted fever and
                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosing typhus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1998-427031/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity 96. 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ching W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5319 BP; 1815 A; 766 C; 983 G; 1755 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         attenuation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                faecalis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              faecalis genome contig SEQ ID NO:202.
                                                        1065-1071;
                                                                                                                                                                                                                                                                                                                                GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                            97US-0066009.
97US-0044031.
97US-0046655.
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91US-0742128.
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                                                                                                                                                                                                                                                                                PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dasch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      computer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig;
                                                     2084pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spotted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 28.4;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dobson ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              readable medium; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterococcal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           layer proteins - useful for preparing vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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XX AACOOL
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XX O6-OCT
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OS Homo s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 22
The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9681 ATGTATAGTAGCTTTTGCTAGAGATA 9656
                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo diagnostic, forensic, gene therapy and chromosome mapping procedu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10996 BP; 3633 A; 1848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          982 nucleotide sequences isolated from the Enterococcus faecalis aax12938 to aax13919 represent these nucleotide sequences which a
                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dumas Milne Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC00105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC00105 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 atttataggagctattgctacagata 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-500381/45.
DB; AAG00099.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 84.0
22; Conservative
                                                                                                                                                                                                                                                                                                                                                                           SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry
                                                                                                                                                                                                                                                                                                                                                                              ID 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; expressed sequence tag; secreted
chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.3%;
                                                                                                                                                                                                                                                                                                                                                                           71pp + CD-ROM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ç
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                                                                                                                                                                                                                                                                                                                                                                              English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO: 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 10996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          procedures
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RESULT 4
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                                                                                                           RNA from cytolytic T cell clone T4T8C1, which expresses high levels of TIA-1 antigen was used for the construction of a cDNA library in lambda gtil. When this expression library was screened using TIA-1 monoclonal antibody, several bacteriophage expressing immunoreactive fusion proteins were identified. Cross hybridisation analysis claentified three independent clones contg. related cDNAs. The largest cDNA insert was used to probe the original library for isolation of full length cDNAs. When this same probe was used to screen a second lambda gtil library prepd. from PHA-activated T cells, a 2.2 kb insert cDNA was isolated, clone 269.4, which encodes rp40-TIA-1, a 40 kD TIA-1 antigen. A segment of the cDNA is useful as a probe for determining the presence of cytolytic lymphocytes in a biological sample. This ability provides an early warning of the cDNA is useful considered to the constant of the cDNA is useful as a probe for determining the presence of cytolytic lymphocytes in a constant of the cDNA is useful as a probe for determining the presence of cytolytic lymphocytes in a cytoly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 35; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anderson PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antigen; cytolytic lymphocyte; infection; HIV; targetting; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA encoding rp40-TIA-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAY-1993 (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ34554 standard; cDNA; 2228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding TIA-1 antigen - used for detecting and cytotoxic killing of cytolytic lymphocyte(s) applicable for cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DAND ) DANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUL-1991;
19-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9301314-A.
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nes 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 catttataggagctattgctacagataca 30
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DB; AAR32009.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schlossman SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91US-0726607.
92US-0843949.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 57..1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streuli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
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Query Match Best Local Similarity

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RESULT 5
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                                                                                              CC present invention describes M. jannaschil open reading frames from the comme sequence. The invention also describes a computer based system comme sequence. The invention also describes a computer based system components of the M. jannaschil genome that are components of the M. jannaschil genome that are components of the m. jannaschil genome that are components of the modelogous to target nucleotide sequences, comprising: (a) data storage means comprising the nucleotide sequence of the 164976, 58407 or 16550 componence at least 99.98 identical to it; (b) search means for comparing a componence at least 99.98 identical to it; (b) search means for obtaining components sequence to the nucleotide sequence of the data storage means to component in the means for obtaining components of identify a homologous sequence, and (c) retrieval means for obtaining components of the homologous sequence. The method, which is based on whole genome components of an autotrophic archaeon M. jannaschil, the genome components of the 164976 bp sequence given in AAV21209), and controlled the components of the 164976 bp sequence given in AAV21210), and controlled the components of the sequence given in AAV21210), and controlled the components of the components of the sequence given in AAV21210), and controlled the components of the sequence given in AAV21210), and controlled the components of the sequence given in AAV21210), and controlled the components of the sequence given in AAV21210), and controlled the components of the sequence given in AAV21210), and controlled the components of the sequence given in AAV21210), and controlled the sequence given in AAV21210).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; Page 152-585; 614pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bult CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methanococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV21209 standard; DNA; 1664976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents the complete 1.66-megabase pair genome sequence of the Methanococcus jannaschil circular chromosome. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete genome sequence of methano-genic archaeon, Methanoccoccus jannaschii - useful in identification of M. jannaschii genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENO-) INST GENOMIC RES.
(UNII ) UNIV ILLINOIS FOUND.
(UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
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79.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter JC,
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Pred. No. 31
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RESULT 7
AAZ29770/c
ID AAZ297
XX
AC AAZ297
XX
DT 27-MAR
XX
DE POTATO
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                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to isolated and purified cDNA encoding a human hydrolase-like molecule (HHLM), designated HHLM-1 to HHLM-8. The HHLM DNAs and polypeptides are useful for diagnosing, treating or preventing cell proliferation disorders and autoimmune disorders. Cell proliferation disorders and autoimmune disorders include AIDS (acquired immune deficiency syndrome). The present sequence
       Potato alpha-amylase gene promoter
                                          27-MAR-2000
                                                                           AAZ29770;
                                                                                                          AA229770 standard;
                                                                                                                                                                                         1815 tttttagaagctattgggacagattca 1841
                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Column 57-58; 38pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proliferation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase-like molecule; human; cell proliferation disorder; autoimmune; cancer; AIDS; acquired immune deficiency syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human hydrolase-like molcule 1 cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human hydrolase-like molecules (HHLMs) and polynucleotides encoding HHLMs, useful for diagnosing, treating or preventing cell liferation (e.g. bone cancer) or autoimmune disorders(e.g. AIDS or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             σ
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DB; AAB28790.
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                                                                                                                                                                                                                                                                                                                                                                              encoding a HHLM protein of the invention.
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                                          (first entry)
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                                                                                                          DNA; 1114
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                                                                                                                                                                                                                                                                          63.3%;
81.5%;
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Pred. No. 45;
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AAT30126/c
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Best Local
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04-JUN-1998;
25-SEP-1998;
25-SEP-1998;
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                                                                                                            08-JAN-1997
                                                                                                                                                                               AAT30126 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1114 BP;
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                                                                           Alpha-amylase 1 promoter
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                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                            (first entry)
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98AU-0006169.
98AU-0006174.
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                                                                                                                                                                                                                                                                                                                                                                                                                   326
                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                62.78;
76.78;
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                                                                                                                                                                                 ВP
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Potato alpha-amylase promoter sequence; alpha-amylase; phenotype modulating genetic sequence; PMGs; transposon tagging; ps element; dissociation element; UQ406 sequence; starch metabolism; plant pathogen resistance; senescence timing; cell growth; ds.
                                                               Location/Qualifiers 647..654
/*tag= a
/note= "UQ406 insertion with single
      Ds
      element"
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New polynucleotides that increase gene expression in plants used produce transgenic plants with resistance to plant pathogens  $\boldsymbol{\cdot}$ ៥

The present sequence is potato alpha-amylase promoter sequence. This shows strong similarity to an alpha-amylase promoter of tomato. The manipulation of amylase levels is done by introducing isolated phenotype modulating genetic sequence which increases or stabilizes expression of a second nucleotide sequence inserted proximally. GenomeWalker (14) is used to clone tomato DNA sequences flanking the Ds element in UQ406. The Ds sequence inserts into the promoter region. This is used in transposon tagging of alpha-amylase gene to identify mutants exhibiting altered physiological properties. Transgenic plants having altered phenotypic traits, such as resistance to plant pathogens, senescence timing, starch metabolism, cell growth, expansion and/or division, and the shape of cells, tissues or organs can be produced.

Score 18.8; D Mismatches DΒ 7; Indels Length 1114; 0 Gaps

0

16 30

Alpha-amylase 1; amy 1; promoter; plant; enzyme; starch breakdown; tuber; reducing sugar; potato; sprout; stem tissue; dicotyledonous plant; agrobacterium; crop protein; nutrition; mammal; interferon; insulin;

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RESULT
AAV02872/
ID AAV0
XX
AC AAV0
XX
DT 28-A
XX
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                                                                                                                                                mest Local
                                                                                                                                                                                                                        This sequence represents the Solanum tuberosum alpha-amylase 1 promoter. CC Alpha-amylase is one of the key plant enzymes, and participates in the CC pathway responsible for the breakdown of starch to reducing sugars in CC potato tubers. Alpha-amylase is encoded by a gene family consisting of CC at least five individual genes divided into two sub families (the type 1 cand type 3 alpha amylases). Type 1 alpha-amylases are expressed in CC sprout and stem tissues, but not in tubers, roots or leaves. The type 3 alpha amylases are expressed in tubers, sprouts and stem tissues. The CC promoter is used to direct expression of a gene of interest in stem CC calls, tissues or organs of a dicotyledonous plant (such as a potato). This sequence can be used in constructs, such as vectors (such as those CC derived from agrobacterium), for transforming cells to express a gene of interest. The gene of interest that is fused to this promoter sequence CC may be a crop protein gene with an optimised amno acid composition, so CC as to increase the nutritive value of the crop. It is also possible to use this promoter to express non-plant genes for mammalian products, such as interferons, insulin, blood factors, and plasminogen activators.
                                                                                                                                                                Query Match
Best Local
                                                                                                          1025
                                                      )872/c
AAV02872 standard;
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            28-APR-1998
                                  AAV02872;
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant alpha-amylase gene promoter - capable of expressing a gene interest in sprout or stem tissue of a dicotyledonous plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-230612/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DANI-) DANISCO AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-OCT-1994;
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                                                                                                          factor; plasminogen activator; ss
                                                                                                                                                   ch 62.7%;
l Similarity 76.7%;
23; Conservative
                                                                                                                                                                                                        2094 BP; 618 A; 357 C; 369 G; 750 T; 0 other;
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             (first entry)
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1863.1866
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                                                       CDNA; 2556
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7..1932
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0; Mismatches
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RESULT 10
AAZ90465/c
ID AAZ904
XX AAZ904
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Best Local Similarity
Matches 23; Conserv
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            antiinflammatory;
                                                                           06-JUN-2000
                                                                                                AAZ90465;
                                                                                                                    AAZ90465 standard; DNA;
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                                                      Transcription
                                                                                                                                                                                                                                                                       Sequence 2556 BP;
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                                                                          (first
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             virucide;
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                                                                          entry)
                                                                                                                                                                                                                             62.7%;
76.7%;
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This cDNA sequence encodes a human tata-binding protein associated factor, hTAFII105, isolated from Daudi cell nuclear extracts. Tightly associated subunits (TAF's) are components of the transcription factor TFIID and are thought to mediate transcriptional activation. This encoded protein may be produced recombinantly from transformed host cells or purified from human cells. hTAFII105 specific binding agents such as specific antibodies could be used for diagnosis (e.g. genetic hybridisation screens for hTAFII105 transcripts), therapy (e.g. gene therapy to modulate hTAFII105 gene expression) and in the biopharmaceutical industry (e.g. as immunogens, reagents for isolating B cell specific activators or other transcriptional regulators).
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TATA box-binding protein associated factor II 105; TAFIII105; cancer; transcription factor; apoptosis; cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding human tata-binding protein associated factor - producing recombinant protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        974 ACAGTTCTGGGTGCTGTTGCTCCAGAAACA 945
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                                                                                                        factor subunit TAFII105 polypeptide encoding DNA
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/product- hTAFII105
/note- "human tata binding protein associated
/note- factor 105 partial sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18.8;
Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                             Human latent transforming growth factor-beta binding protein 3; hLTBP-3; TGF-beta inhibitor; proliferative; anti-proliferative; cytostatic; cardiant; anti-inflammatory; cerebroprotective; immunosuppressive; thrombolytic; osteopathic; vulnerary; tranquilizer; antibacterial; PAI-1; plasminogen activator inhibitor-1; thrombomodulin; tissue growth; tumour; prevention; treatment; cancer; fibrosis; dilated cardiomyopathy; injury; osteoporosis; myocardial infarction; congestive heart failure; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This DNA encodes a polypeptide comprising a (modified) fragment (I) of a TATA box-binding protein associated factor II 105 (TAFII105). A pharmaceutical composition comprising (I) or the polynucleotide or an inhibitor or antagonist of (I) is useful for treating cancers and inducing apoptosis in pathological cells. The composition is also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ51928 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            negative effect on protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptide encoding TATA box binding protein associated factor II 105 useful for treating e.g. cancers and inducing apoptosis has a dominant negative effect on the normal biological activity of the binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dikstein R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-1998;
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                                                                                                                                            thrombosis; stroke; systemic inflammatory response syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ51928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Fig 1; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAY57279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for treating autoimmune diseases, inflammatory processes and viral or bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        974
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                                                                                     sepsis syndrome; multiple organ ic plaque rupture; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 797 A; 614 C; 514 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98IL-0125971.
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/transl_except= (pos: 2499..2501, aa: Glx)
/note= "the stop codon is not indicated"
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1..2556
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76.78;
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                                                                                                                                                                                                                                                                                                                                                                                            growth factor-beta binding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ₽P
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Pred. No. 5
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                                                                                                               dysfunction syndrome,
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                                                                                                                                                                                                                                                                                                                                                                                         3 (I) gene.
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Homo sapiens

Human latent transforming growth factor-beta binding protein 3; hLTBP-3;

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RESULT 12
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ID AAZ519
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                                                        Human latent transforming growth factor-beta binding protein 3 (II) gene.
                                                                                                                                                                                                                                                                                                                                                                                                2406 ACATCTGTAGGAGCCATTGGTATTGATGCA 2377
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                                                                                                                      04-JUL-2000
                                                                                                                                                                                  AAZ51929;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3624 BP;
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/product= "hLTBP-3"
/note= "Does not include stop codon"
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Pred. No. 5
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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                   activity, TGF-beta secretion and cellular proliferation. Modulation of hITBP-3 is useful for prevention and/or treatment of diseases arising from cellular effects induced by TGF-beta, especially cancer, fibrosis, osteoporosis, myocardial infarction, congestive heart failure, dilated cardiomyopathy, deep venous thrombosis, disseminated intravascular thrombosis, stroke, sepsis, injuriosis, disseminated intravascular thrombosis, stroke, sepsis, injuriosis proliving major tissue damage and trauma, systemic inflammatory response syndrome, sepsis syndrome, sepsis syndrome, multiple organ dysfunction syndrome, and atherosclerotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a gene encoding human latent transforming growth factor (TGF)-beta binding protein 3 (hLTBP-3). The gene was obtained by reverse transcriptase PCR of mRNA isolated from hLTBP-3 expressing tissues e.g. cartilage, bone, brain, kidney, ovary, pancreas, stomach and spleen. The protein is often co-expressed with TGF-beta and functions as its inhibitor. hLTBP-3 is useful for inhibiting or stimulating tissue growth in vitro or in vivo and for inhibiting tumour growth. The hLTBP-3 or its homologues, and antisense nucleic acid sequences can be used to regulate TGF-beta activity, especially plasminogen activator inhibitor-1 expression, activity or secretion, thrombomodulin expression or
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   2553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human latent transforming growth factor (TGF)-beta binding protein 3, nucleic acids and vectors useful as modulators of TGF-beta, for inhibiting tissue or tumor growth, and treating e.g. osteoporosis and myocardial infarction -
                                                                                                                                                                                                                                                                                                                           Sequence
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53 ACATCTGTAGGAGCCATTGGTATTGATGCA
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                                                                                                                                                l Similarity
23; Conserv
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                                                                                                                                                                                                                                                                                                                       676 A; 1297 C; 1209 G;
                                                                                                                                                                              62.7%;
76.7%;
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                                                                                                                                                                          Score 18.8;
Pred. No. 59;
                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                       0 other
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Homo sapiens

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AAF28253/c
ID AAF28253 standard; DNA; 3867 BF
XX
AC AAF28253;
XX
DT 04-APR-2001 (first entry)
XX
DE Human TANGO; colon; inflammati
XX
TANGO; MANGO; colon; inflammati
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Human TANGO; colon; inflammati
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DE Human TANGO; colon; inflammati
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DS Homo sapiens.
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DA WO200100672-Al.
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29-JUN-1999; 99US-0342687.
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PY
29-JUN-1999; 99US-0342687.
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PR
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DA (MILL-) MILLENNIUM PHARM INC.
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DR WPI; 2001-050127/06.
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RRSULT 1
AAF28251
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XX AAF2
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2508
                                                                                     TANGO; MANGO; colon; inflammation; tumor; renal; liver; lung;
autoimmune; allergy; cardiovascular; brain; degenerative; pla
pancreatic; skeletal; muscle; ss.
                                                                                                                                                                                                                                                                   04-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins. The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle
                                                                                                                                                                                                         Human TANGO 275 DNA
                                                                                                                                                                                                                                                                                                                                                                                 AAF28252 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and live
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 acatttataggagctattgctacagataca 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACATCTGTAGGAGCCATTGGTATTGATGCA 2479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 670 A; 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.7%;
76.7%;
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Pred. No. 59;
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Matches 23; Conserv
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06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins. The nucleic acids, proteins and protein modulators are useful for treating colonic disorders, inflammatory diseases, tumors, renal disorders, liver disorders, lung disorders, autoimmune diseases, allergic diseases, cardiovascular diseases, brain disorders, degenerative diseases placental, pancreatic, skeletal and muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated cDNAs encoding TANGO 244, TANGO 246, TANGO 275, TANGO 300 and MANGO 245 proteins, useful in the treatment of inflammatory diseases (e.g. idiopathic ulcerative colitis), tumors, renal disorders and lived disorders (e.g. jaundice) -
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                                                         WPI; 1999-045171/04
                                                                                                              Barash SC,
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                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9850555-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus faecalis genome contig SEQ ID NO:276
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                                                                                                           Dillon PJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         faecalis; contig; detection; Enterococcal infection;
enuation; computer readable medium; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                              97US-0066009.
97US-0044031.
97US-0046655.
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                                                                                                                                                                                                                                                                                                                             98WO-US08985
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                                                                                                              Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20633
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Pred. No. 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         665 T; 0 other;
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A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAXI2938 to AAXI3919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in a animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 1284-1294; 2084pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
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Query Match Best Local S Matches 23 Local Similarity mes 23; Conserv Conservative 62.78; 76.78; 0 Score 18.8; Pred. No. 74; Mismatches DB 20; 7; Indels Length 20633 0 Gaps 0

Sequence 20633 BP; 5857 A; 4284 C;

3025 G; 7427 T;

40 other;

õ 14803 acattaatagcatctaatgtgccagataca 14832 L acatttataggagctattgctacagataca 30

Search completed: September 28, Job time: 1553 sec 2001, 10:26:07 THIS PAGE BLANK (USPTO)

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Maximum Match 100%
Listing first 45 summaries
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     seq length: 0 seq length: 2000000000
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Match
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1: /cgn1_7/ptodata/1/ina/5A_COMB.seq:*
2: /cgn1_7/ptodata/1/ina/5B_COMB.seq:*
3: /cgn1_7/ptodata/1/ina/6A_COMB.seq:*
4: /cgn1_7/ptodata/1/ina/6B_COMB.seq:*
5: /cgn1_7/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn1_7/ptodata/1/ina/backfiles1.seq:*
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US-07-843-949A-1
US-07-843-949A-3
US-08-218-978-1
US-08-218-978-3
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US-08-246-403A-13
US-08-265-315-42
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US-09-265-315-42
US-09-265-315-7
US-08-444-903A-1
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OB-169-927-1  OB-169-927-1  OB-169-927-1  equence 1, Application US/0816992  atent No. 5783441  APPLICANT: Carl, Mitchell  APPLICANT: Cobson, Michael E.  APPLICANT: Dobson, Michael E.  APPLICANT: Dobson, Michael E.  APPLICANT: Dobson, Michael E.  APPLICANT: Dobson, Michael E.  APPLICANT: Ching, Wei Mei Mei  APPLICANT: Dobson, Michael E.  APPLICANT: Ching, Wei Mei Mei  TITLE OF INVENTION: Gene and F  TITLE OF INVENTION: Preparation  TYPE: HIGH TYPE: Proppy disk  COUNTRY: USA  TITLE COMPUTER: IBM PC Compatible  OPERATING SYSTEM: PC COMPATION  APPLICATION NUMBER: US/08/16  FILING DATE: OS/09/91  ATTORNEY/AGENT INFORMATION:  APPLICATION NUMBER: US/08/16  FRICH APPLICATIO	557.3 557.3 556.0 566.0 566.0
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ORIGINAL SOURCE:

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Best Local Similarity
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OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4183 ACATTTGTAGGAGCTATTGCTACAGATACA 4212
                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICATION NUMBER: 07/460,678 FILING DATE: January 5, 1990 ATTORNEY/AGENT INFORMATION:
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CITY: Boston
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LOCATION:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE: Characterization of the gene encoding the TITLE: protective S-layer protein of Rickettsia TITLE: prowazeki; presence of a truncated identical TITLE: homolog in rickettsia typhi JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
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STRAIN: Breinl
                                                                        APPLICATION NUMBER: US/07/FILING DATE: July 10, 1991
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Ching, W. M.
Dasch, G. A.
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379..386
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US-07-843-949A-1/c
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Best Local Similarity 79.3%;
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                APPLICATION NUMBER: 07/7
FILING DATE: July 10, 19
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Jante V
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
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TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Anderson, Paul APPLICANT: Streuli, Michel APPLICANT: Schlossman, Stu
                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                     REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
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                                         LENGTH:
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VENTION: DNAS ENCODING PROTEINS ACTIVE IN
VENTION: LIMPHOCYTE-WEDIATED CYTOTOXICITY
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linear
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Pred. No. 10;
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US-09-013-881-9; Sequence 9, Application US/09013881
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US-08-218-978-1/c
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Best Local Similarity
Matches 23; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/460,678
FILING DATE: January 5, 1990
APPLICATION NUMBER: 07/726,607
FILING DATE: July 10, 1991
ATTORNEY_AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
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                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
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ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Schlossman, Stuart F.
TITLE OF INVENTION: DNAS ENCODING PROTEINS ACTIVE IN
TITLE OF INVENTION: LYMPHOCYTE-MEDIATED CYTOTOXICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Streuli, Michel APPLICANT: Schlossman, Stu
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                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
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STATE: Massa
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                                                                                 CATTCATAGCAGCTAATGCTGCAGCTGCA 230
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                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                  linear
                                                                                                                                                              64.7%;
79.3%;
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79.38;
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Pred. No. 10;
0; Mismatches
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                                                                                                                                                              Score 19.4;
Pred. No. 1
                                                                                                                                                 Mismatches
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                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                    APPLICANT: Dikstein, Rivka
APPLICANT: Tjian, Robert
TITLE OF INVENTION: B-Cell Specific Transcription Factor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett.
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                    1815 TTTTTAGAAGCTATTGGGACAGATTCA 1841
                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
LIBRARY: PITUN
CLONE: 094168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2162 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Guegla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                             STREET:
                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
COUNTRY: USA
                                                            ADDRESSEE:
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                           SSEE: SCIENCE & TECHNOLOGY LAW GROUP
T: 268 BUSH STREET, SUITE 3200
SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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              CALIFORNIA
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Corley, Neil C.
Guegler, Karl J.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PITUNOT01
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IBM Compatible
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Pred. No.
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NAME/KEY:
; LOCATION:
US-08-725-012-1
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50z or 55SX
COMPUTER: IBM PS/2 Model 50z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOSTWARE: WOODPERFECT (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/843,949A
FILING DATE: 19920219
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/460,678
APPLICATION NUMBER: 07/460,678
FILING DATE: January 5, 1990
APPLICATION NUMBER: 07/726,607
FILING DATE: JULY 10, 1991
ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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LENGTH: 2556 base pairs
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NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Streul1, Michel
APPLICANT: Schlossman, Stuart F.
TITLE OF INVENTION: DNAS ENCODING PROTEINS ACTIVE IN
TITLE OF INVENTION: LYMPHOCYTE-MEDIATED CYTOTOXICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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CITY: Boston
STATE: Massac
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: double
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 02110-2804
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Pred. No. 19;
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Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                     TELEPHONE: (617) 542-8906
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                    APPLICATION NUMBER: 07,843,949
FILING DATE: February 19, 1992
APPLICATION NUMBER: 07,460,678
FILING DATE: January 5, 1990
APPLICATION NUMBER: 07,726,607
FILING DATE: July 10, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/218,978
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MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                   TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                   SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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                                                                                                                                                                      NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/021003
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ZIP: 02110-2804
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                 STRANDEDNESS:
                                   TYPE:
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TOPOLOGY:
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225 Franklin Street
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Schlossman, Stuart F.
Schlossman, Stuart F.
VENTION: DNAS ENCODING PROTEINS ACTIVE IN
VENTION: LYMPHOCYTE-MEDIATED CYTOTOXICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anderson,
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75.9%;
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Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.44 Mb
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OTHER INFORMATION: ,
OTHER INFORMATION: K
US-08-246-403A-13
                                                                                                                                                           Query Match
Best Local Similarity
Watches 21; Conserve
                                                       US-08-714-918-42/c
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US-08-246-403A-13
                         Sequence 42, Application US/08714918 Patent No. 6037123
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                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Kaji, Akira
                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 703-205-8050 INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1861 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Svensson, Leonard |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Mutation of RepA Protein NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                          133 ATAGTGATAGAGGCTATTGGTACAGAT 159
                                                                                                                                                                                                                                                                                                                                    OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 CATTCATAGCAGCTAATGCAGCAGCTGCA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 20-MAY-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Svensson, Leonard R. REGISTRATION NUMBER: 30330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                  1 acatttataggagctattgctacagat 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 catttataggagctattgctacagataca 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
                                                                                                                                                                          Conservative
Benton, Bret
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birch, Stewart, Kolasch & Birch
                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                              both
                                                                                                                                                                                      58.0%;
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75.9%;
                                                                                                                                                                                                                                                           /note= "replication portion of
Rts1, see Fig. 12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30330
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                                                                                                                                                                                      Score 17.4;
Pred. No. 68;
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Pred. No. 45;
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US-09-265-315-42/c; Sequence 42, App.; Patent No. 61875;
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Best Local Similarity
Matches 21; Conservi
                                                                                                                                                                                                                                                       RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2119 base pair
                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                               APPLICANT:
APPLICANT:
                              APPLICANT: Sun, Dongxu
TITLE OF INVENTION: MET
TITLE OF INVENTION: ACT
TITLE OF INVENTION: TAN
                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL TITLE OF INVENTION: TARGET GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                         446 TTTAAAATAGCTTTTCCTACAGATAAA 420
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TELEFAX: (213) 955-0440
TELEX: 67-3510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
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6187541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2119 base pairs
                                                                                             Lee, Ving J.
Malouin, Francois
Martin, Patrick K.
Schmid, Molly B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              633 West Fifth Street
                                                                                                                                                                  Benton, Bret
                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Martin, Patrick K.
Schmid, Molly B.
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September 13, 1996
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                            METHODS OF SCREENING FOR COMPOUNDS ACTIVE ON STAPHYLOCOCCUS AUREUS TARGET GENES
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77.8%;
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Pred. No. 70;
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STREET: 633 West Fifth Street STREET: Suite 4700

Los Angeles : California

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TOPOLOGY: US-09-265-315-42
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Best Local Similarity
Matches 21; Conserv
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   -09-265-315-42/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
AFTIONNEY/AGENT INFORMATION:
NAME: WAITBULTS, Richard J.
PROCESSMERTEN, NUMBER: 32,77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 42: SEQUENCE CHARACTERISTICS: LENGTH: 2119 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 tent No.
                                                                                                                                                                   TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS TITLE OF INVENTION: TARGET GENES NUMBER OF SEQUENCES: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                  APPLICANT:
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ZIP: 90071-2066
COMPUTER READABLE FORM:
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                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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TELEX: 67-3510
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                                                                                                                                                                                                                                          Martin, Patrick K.
Schmid, Molly B.
Sun, Dongxu
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Malouin, Francois
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77.8%;
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Pred. No. 70;
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US-09-265-315-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C.
SOFTWARE: WOR'D Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/:
                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2119 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                 APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                               STREET: Suite 4700
CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: September 13, APPLICATION NUMBER: 60/009 FILING DATE: December 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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MEDIUM TYPE:
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633 West Fifth Street
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Martin, Patrick K.
Schmid, Molly B.
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uin, Francois
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77.8%;
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mber 13, 1996
60/009,102
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 US/09/266,417
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Pred. No. 70;
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                                                   DOS 5.0
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PRIOR APPLICATION DATA:

08/714,918

March 9, 1999

FILING DATE: APPLICATION NUMBER: CLASSIFICATION:

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; TOPOLOGY: US-09-266-417-42
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Best Local Similarity
Matches 21; Conser
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REFERENCE/DOCKET NUMBER: 240/:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
TELEX: 67-3510
                                                                                       TELEFAX: 703-205-8050 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30330
                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 20-MAY-199
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TITLE OF INVENTION: Mutation of RepA Protein
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                         REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION: 703-205-8000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        446 TTTAAAATAGCTTTTCCTACAGATAAA 420
                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
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                                   STRANDEDNESS:
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                                                   nucleic acid
                                                                  3356 base pairs
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IUMBER: 60/009,102
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77.8%;
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Pred. No. 70;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
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OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION:
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                                                    Local
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T: P.O. Box 747
Falls Church
                                   Similarity 77.0
21; Conservative
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77.8%;
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77.8%;
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                                     Score 17.4; E
Pred. No. 74;
0; Mismatches
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Search completed: September 28, 2001, 10:23:38 Job time: 1404 sec

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Minimum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1117: 1120:

Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being part and is derived by analysis of the total score distribution. printed, co

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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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AQ462588
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Eukaryota; Metazoa; C
Mammalia; Eutheria; I
1 (bases 1 to 449)
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HS_5205_A2_C11_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=781 Col=22 Row=E, DNA sequence.
                               Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
 Sequence-tagged connectors: A sequence approach to mapping and
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Primates;
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                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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AV208558
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AL194034 Tetraodon
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AW738482 EST339909
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                          Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                              University of Utah University of Utah Rm. 308, Biomedical
                                                                                                             Unpublished (2000)
Contact: Robert B.
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Class: BAC ends
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                                                                                                                                                            Mouse whole genome
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Email: ddunn@genet1cs.utah.edu
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24; Conservative
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Rodentia;
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-387
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 781 row: E column: 22
                                                                                                                                                      Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ821630 580 bp DNA GSS 2M0094B03R Mouse 10kb plasmid UUGC1M library Mus clone UUGC2M0094B03 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the BBACe3.6 vector at EcoRI sites "

70 c 53 g 199 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=781 Col=22 Row=E"
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                                                                                                                                          scaffolding with paired
Polymers Research
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Pred. No. 98;
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- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org.The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of
                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNS00G9G 1101 bp DNA GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR32E08 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                           Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                   Genoscope.
Direct Submission
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory Mouse DNA Resource
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/clone="UUGC2M0094B03"
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
plate: LLCM949 row: p column: 12
High quality sequence stop: 226.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Eukaryota; M
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NIH-MGC http://mgc.nci.nih.gov/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/tisue_type="carcinoma, cell line"
/tab host="DH10B (Tl phage-resistant)"
/note="Organ: bladder; Vector: pDNR-LIB (Clontech);
/note="Organ: bladder; Vector: pDNR-LIB (Clontech);
/note="Organ: bladder; Vector: pDNR-LIB (Clontech);
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/db_xref-"taxon:7227"
/clone_lib-"RPCI-98"
/clone="BACR32E08"
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229 c 236 g
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/clone_lib="NIH_MGC_53"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.3e+02;
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                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 307 row: A column: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-307A9.TJ
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RPCI-23-307A9.TV F
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,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M.,
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1 (bases 1 to 376)
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                      /lab_host="DH10B"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
a 53 c 99 g 89 t
                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="RPCI-23-307A9"
                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                       /sex="Female"
                                                                                                                                                                                                                                                                                                                        /clone_lib="RPCI-23"
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82.1%;
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Pred. No.
                                                   Score 20; DB 236;
Pred. No. 1.4e+02;
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                                                                                            BF394068 589 bp mRNA EST 27-
UI-R-CAO-bgy-f-08-0-UI.S1 UI-R-CAO Rattus norvegicus
UI-R-CAO-bgy-f-08-0-UI 3', mRNA sequence.
BF394068
BF394068.1 GI:11378932
Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     van der Hoeven,R.S., Bezzeredes,J.L., Matern,A.L., Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Glovannoni,J.J. and Tanksley,S.D. Generation of ESTs from tomato flower tissue, anthesis
                                                           Norway rat.
                                                                                 EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clemson University
100 Jordan Hall, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST
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                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="flower"
/tissue_type="flower"
/dev_stage="anthesis"
/note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="tomato flower buds, anthesis, Cornell
University"
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/clone="cTOD7016"
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82.1%;
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Pred. No. 1.5e
0; Mismatches
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   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
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1.5e+02;
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Cornell University
7016 5', mRNA sequence
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The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-92, >BCl_MM#scRNA 343-589, >RMER16#LTR
Seq primer: M13 FOrward
                         1 (bases 1 to 421)
Hillar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., I Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., R., Williamson,A., Wohldmann,P. and Wilson,R.
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yq98c11.r1 Soares fetal
IMAGE:203828 5' similar
                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
H56427
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Tel: 319 335 8250
Fax: 319 335 9565
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University of Iowa
451 Eckstein Medical Research Building Iow
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Bonaldo, M.F., Lenno
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/db_xref="taxon:10116"
/clone="UI-R-CA0-bgy-f-08-0-UI"
/clone="UI-R-CA0"
/lab_host="DH108 [Life Technologies]"
/note="Vector: pT773D-Pac (Pharmacia) with a modified
/note="Vector: pT773D-Pac (Ph
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129 c
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98 g
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liver spleen lNFLS Homo sapiens cDNA clone
to contains Alu repetitive element;, mRNA
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1.5e+02;
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RESULT 9
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                                                                       l (bases 1 to 444)

l (bases 1 to 444)

shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theisding,B., Allen,M., Bowers Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann Public Soybean EST Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                              AW395142 444 bp mRNA ES9 sh40d08.yl Gm-c1017 Glycine max cDNA clone Gm-c1017-4168 5', mRNA sequence.
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High quality sequence stops: 355
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RP1
                    Public Soybean EST Project
Washington University School of Medicine
                                                        Contact: Shoemaker R/Public Soybean EST Project
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Contact: Wilson RK
                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
                                                                                                                                                                                                                                                                                                                                       soybean.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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/clone="IMAGE:203828"
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/db_xref="GDB:3772959"
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Tetraodon nigroviridis.

Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Tetraodon.

1 (bases 1 to 494)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.

Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tetraodon nigroviridis genome survey sequence PUC-Ori end of c 262L12 of library G from Tetraodon nigroviridis, genomic surve sequence.
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Tetraodon nigroviridis DNA sequence Unpublished
                                              Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetier,F., Saurin,W. and Weissenbach,J.

Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                        Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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Location/Qualifiers
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                                                                                                                                                          (bases 1 to 494)
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/db_xref="taxon:3847"
/clone="cenome SYSTEMS CLONE ID: Gm-c1017-4168"
/clone_lib="Gm-c1017"
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/lab_host="XL10-Gold"
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Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a lauscale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                        Contact: Zeguang Han Chinese National Human Genome Center at Shanghai Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45) Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                       Peng,Y., Song,H., Huang,Q., Huang,C., Gu,Y., Yang,Y., Gao,G., Xi,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., L.,G., Hu,R., Chen,J., Chen,Z. and Han,Z.
Homo sapiens cDNA ADC clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 577)
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                185
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clone is available at CHGC in
Location/Qualifiers
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PUC-Or1"
104 c 135 g 108 t 5 others
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/db_xref="taxon:99883"
/clone="262112"
                                                                   /tissue_type="Adrenal gland"
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                        /clone_lib-"ADC"
                                                                                                                                         /clone-"ADCAYC1
                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 2.2e+02;
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65.3%;

Score 19.6; DB 32 Pred. No. 2.2e+02;

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**AL Unpublished (1999)

**Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center, The Tatitite of Phenomes and Phenomes Science Laboratory
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CDNA clone 1700109E04 3', mRNA sequence.
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URL:http://genome.rtc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      visit our web site (http://genome.rtc.riken.go.jp) for
              /note="Site_1: XhoI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
                                                                                                                                                                                      /tissue_type="testis"
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Hayashizaki
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The Institute of Physical and Chemical Research (RIKEN), Genomi
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URL:http://genome.rtc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
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Tel: +81-298-36-9013
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                                                   visit our web site (http://genome.rtc.riken.go.jp) for
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
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,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 323)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Class: plasmid ends
High quality sequence stop: 323
Location/Qualifiers
                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0134 row: F column: 07
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                      plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ838439 323 bp DNA GSS 20-FEB-2001 2M0134F07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0134F07 F, DNA sequence.
                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                              Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ838439.1
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                                                                                                                                                                                                                    Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

29 c 47 g 101 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-*Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
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/clone="4930419L17"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RIKEN full-length enriched, adult male testis
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79.38;
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Pred. No. 2.5e+02;
                                                                                                          Std Error: 0.00
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA973786 325 bp mRNA EST 07-JUL-1998 oq16d10.sl NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1586515 3 similar to gb:M77142 NUCLEOLYSIN TIA-1 (HUMAN);, mRNA sequence.
Trace considered overall poor quality Insert Length: 917 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1.
                                                                                                                CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwp42 (gil4732114|gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86
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musculus C57BL/6J (male) was obtained fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:3148966
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Pred. No. 2.6e+02;
0; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                      Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                        Ph.D.,
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                      Score
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seq length:
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49
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/cgnl_7/ptodata/1/paa/US086_COMB.pep:*
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/cgnl_7/ptodata/1/paa/US090_COMB.pep:*
/cgnl_7/ptodata/1/paa/US090_COMB.pep:*
/cgnl_7/ptodata/1/paa/US096_COMB.pep:*
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                     7 US-99-328-352-8661

US-09-489-039A-9118

US-09-191-989-4

US-09-438-185-284

US-09-489-039A-10840

US-09-417-507-34454

US-09-134-000-5423
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Sequence 1, Appli
Sequence 2, Appli
Sequence 6861, Ap
Sequence 9118, Ap
Sequence 244, Appli
Sequence 10840, A
Sequence 34454, A
Sequence 5423, Ap
Sequence 5423, Ap
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	5	<u>ب</u>	5	5	5	5	5	5	65.3	<u>ر</u>	5.	5	5	5	5	5	5	<u>ب</u>	5	5	7.	.7	7.	7.	7.	7.	7.	7.	7.	7.	7.	7.	7.	7.	7.
	297	282	271	253	253	252	252	252	197	195	193	190	186	161	113	113	113	85	60	58	615	615	558	558	531	531	531	504	342	342	342	342	308	212	173
	Р	16	16	18	18	18	18	18	18	23	23	23	23	23	23	23	23	-	23	ب	23	23	16	16	17	17	17	18	23	23	23	23	16	18	18
	-29963-4	-252-991A-2942	-09-252-991A-	-09-450-651A-47	-09-450-651A-4	-09-450-651A-4	-09-450-6	-09-450-651A-4	-09-417-507	-60-196-713	-60-182-093	-60-196-714	-60-196-718	-60-195-136	-60-169-867	-60-169-842	-60-169-841	S01-0066	-60-169-840	-US01-00663	-60-191-637	0-16	-09-252-691C-8	-09-252-691-896	-09-380-420C-	-09-380-420B-	-09-3	-09-489-039A-14	-60-191-681-154	-60-191-637-195	-60-173-464-160	S-60-167-217-1	S-09-252-991A-18	-09-417-507-3	Ç
	Sequence 46, Appl	294	3051	e 47,	46,	e 45,	e 44,	e 43,	æ	2230	2408	2 700, A	e 7132	1128,	equence 4903,	equence 3089,	equence 1730,	quence 31565,	Sequence 5600, Ap	35001,	21026,	e 745, F	uence 8968,	e 896	uence 2,	uence 2,	uence	e 142	equence 154	e 19589,	e 16064,	e 1967	e 1808	31001,	5

## ALIGNMENTS

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Sequence 1, Application US/09551645

GENERAL INFORMATION:

APPLICANT: HAHM, MYONG-JOON

TITLE OF INVENTION: NEW EPITOPE TAG RECOGNIZED BY A MONOCLONAL ANTIBODY TO

TITLE OF INVENTION: NEW EPITOPE TAG RECOGNIZED BY A MONOCLONAL ANTIBODY TO

TITLE OF INVENTION: NEW EPITOPE TAG RECOGNIZED BY A MONOCLONAL ANTIBODY TO

TITLE OF INVENTION: NEW EPITOPE TAG RECOGNIZED BY A MONOCLONAL ANTIBODY TO

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TITLE OF INVENTION: NEW EPITOPE TAG RECOGNIZED BY A MONOCLONAL ANTIBODY TO

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TOTAL TAG RECOGNIZED BY A MONOCLON
                                                                                                                                                               RESULT 2
US-07-742-128-2
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US-09-551-645-1
Sequence 2, Application US/07742128 GENERAL INFORMATION: APPLICANT: Carl, Mitchell NMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TFIGAIATDT 10
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Pred. No. 0.003;
Mismatches
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Query Match
Best Local Similarity
Thes 7; Conserve
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Best Local Similarity
Watches 9; Conserve
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                                                                                                                                                             ; ORGANISM: Acinetobacter baumannii US-09-328-352-6861
밁
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                                                                                                                                                                                                                                                                                                   Sequence 6861, Application US/09328352
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUWANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                SEQ ID NO 6861
LENGTH: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/742,128
APPLICATION: 19910809
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Spevack, A. David
REGISTRATION NUMBER: 24,743
REFERENCE/DOCKET NUMBER: N.C.72,321
TELEPHONE: (301) 295-6759
TELEPHONE: (301) 295-6759
                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (301) 295-4033:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1612 amino acids
                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1265 TFVGAIATDT 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: AMINO ACID TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20889-5044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TFIGAIATOT 10
                                   2 FIGAIATD 9
 FIGVIATD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Counsel, Naval Medical Res & Dev Cmd National Naval Medical Center
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                                                                      Conservative
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                                                                                      71.48;
87.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.0%;
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                                                                                      Score 35; DB 17
Pred. No. 1e+02;
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Pred. No. 1
                                                                        Mismatches
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1.8;
                                                                                                       DB 17;
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                                                                        Indels
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RESULT 5
US-09-191-989-4
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CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09191989 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9118, Application US/09489039A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 412
                                FILING DATE: May 10, 1994
APPLICATION NUMBER: 08/22
FILING DATE: APPIL 18, 19
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Szasz, Josep
APPLICANT: Davis, Maria
                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                       APPLICATION NUMBER: 08/738,172
FILING DATE: October 25,1996
APPLICATION NUMBER: 08/465,003
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/575,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 TFAGAIAAD 41
REGISTRATION NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 22
                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                               FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TFIGAIATD 9
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                                                                                                                                                                                                                                                                                                                                                                             SYSTEM: IBM P.C. Word Perfect 5.1
                                                                                                                                                        December
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77.8%;
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                                                                                                                                      08/240,158
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  222/158
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Pred. No. 3.1e+02;
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TELEPHONE:

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; ORGANISM: Chlamydia pneumoniae US-09-438-185-284
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                                                                                                                                                                                                                                       US-09-489-039A-10840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Fast SEQ ID NO 284
LENGTH: 482
CURRENT APPLICATION NUMBER: US/09/489,039A CURRENT FILING DATE: 2000-01-27 PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR FILING DATE: 1999-01-29 NUMBER OF SEQ ID NOS: 14342 SEQ ID NO 10840 LENGTH: 567
                                                                                                                           Sequence 10840, Application US/09489039A
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 284, Application US/09438185 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR FILING DATE: 1999-04-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kalman, Sue
APPLICANT: Davis, Ronald
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/438,185
CURRENT FILING DATE: 1999-11-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
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LENGTH: 455 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                            247 FIGAIATLT 255
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Local Similarity 70.0%;
nes 7; Conservative
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nes 8; Conserv
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TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stephens, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : (213) 489-1600
(213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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linear
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018941-000411US
                                                                                                                                                                                                                                                                                                                                                                                                  69.4%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 18;
Pred. No. 3.7e+02;
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Sequence 28277, Application US/09417507

GENERAL INFORMATION:

APPLICANT: KEITH G. WEINSTOCK ET AL.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
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                                                                                                                                           US-09-417-507-28277
                                                                                                                                                                              RESULT
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US-09-134-000-5423
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APPLICANT: KEITH G. WEINSTOCK ET AL.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
TITLE OF INVENTION: FUMICATUS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH99-10
CURRENT APPLICATION NUMBER: US/09/417,507
CURRENT FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 44312
SEQ ID NO 34454
LENGTH: 662
TYPE: PATH TO SERVICE TO S
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CURRENT APPLICATION NUMBER: US/09/134,000A
CURRENT FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 6810
SEQ ID NO 5423
LENGTH: 92
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS
TITLE OF INVENTION: FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
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Best Local S
Matches 7
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Best Local Similarity
Matches 6; Conserv
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Best Local
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les 7; Conservative
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Pred. No.
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Pred. No.
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Pred. No. 5.4e+02;
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RESULT 12
US-09-417-507-31001
US-09-417-507-31001
; Sequence 31001, Application US/09417507
; GENERAL INFORMATION:
APPLICANT: KEITH G. WEINSTOCK ET AL.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
TITLE OF INVENTION: FUNICATUS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH99-10
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Best Local Similarity
""" hes 7; Conserv
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Best Local Similarity
""+ hes 6; Conserv
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US-09-417-507-28277
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Sequence 7555, Application 00,000.

Sequence 7555, Application 00,000.

GENERAL INFORMATION: 00,000.

APPLICANT: Gary Breton et. al APPLICANT: GARY BRETON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
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CURRENT APPLICATION NUMBER: US/09/417,507
CURRENT FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 44312
SEQ ID NO 28277
LENGTH: 110
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 2709, 2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7555
                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/417,507
CURRENT FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 44312
SEQ ID NO 31001
LENGTH: 212
NAME/KEY: UNSURE
LOCATION: (57)
OTHER INFORMATION: Identity of amino acid sequences
-09-417-507-31001
                                                                                                                              TYPE: PRT
                                                                                    FEATURE:
                                                                                                      ORGANISM: A.fumigatus
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87.5%;
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Pred. No. 1.8e+02;
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Pred. No. 1.1e+02;
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Query Match

67.3%;

Score

33; DB 18;

Length

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RESULT 15
US-60-173-464-16064
; Sequence 16064, Application US/60173464
; GENERAL INFORMATION:
; APPLICANT: L1, Peter W.D.
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US-09-252-991A-18081
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US-60-167-217-19670
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APPLICANT: L1, Peter W. D.
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Best Local S
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18081
LENGTH: 308
TYPE: PRT
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LENGTH: 342
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/60/167,217
CURRENT FILING DATE: 1999-11-24
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 23195
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                   319 TFVGSEATD 327
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66.7%;
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Pred. No. 4e+02;
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3.6e+02;
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| Cgnl_7/ptodata/2/paa/PCT_NEW_COMB.pep:*
| Cgnl_7/ptodata/2/paa/US06_NEW_COMB.pep:*
| Cgnl_7/ptodata/2/paa/US07_NEW_COMB.pep:*
| Cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep:*
| Cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep:*
| Cgnl_7/ptodata/2/paa/US08_NEW_COMB.pep:*
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US-09-198-452A-295
US-09-543-681A-6920
US-09-543-681A-6920
US-09-784-676-3000
PCT-USC1-18651-38445
PCT-USC1-08631-31597
PCT-USC1-08631-31597
PCT-USC1-08631-31598
US-09-543-681A-8195
PCT-USC1-08631-53591
PCT-USC1-08631-53
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1376, Ap
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11209, A
15137, A
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Sequence	0 5 US-09-570-581A-1471	500	61.2	30	45
Sequence	7 1 PCT-US01-08631-47697	487	61.2	30	44
Sequence	2 1 PCT-US01-08631-45475	462	61.2	30	<b>4</b> 3
	4 5 US-09-902-540-11688	374	61.2	30	42
		296	61.2	30	41
		176	61.2	30	40
		122	61.2	30	39
	8 5 US-09-834-366-18848	108	61.2	30	38
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		723	63.3	31	31
		628	63.3	31	30
	ഗ	614	63.3	31	29
	5 1 PCT-US01-08631-55097	595	63.3	31	28

ALIGNMENTS

## ; LENGTH: 419 ; TYPE: PRT ; ORGALISM: Arabidopsis thaliana US-09-573-655A-1647 ; ORGANISM: Proteus mirabilis US-09-543-681A-7770 US-09-543-681A-7770 밁 QY ; Sequence 1647, Application US/09573655A ; GENERAL INFORMATION: ; APPLICANT: SOLOVYEV, Victor and TROUKHAN, Maxim US-09-573-655A-1647 Sequence 7770, Application US/09543681A GENERAL INFORMATION: APPLICANT: GARY BRETON APPLICANT: GARY BRETON TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRA TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.1002-001 CURRENT APPLICATION UMBER: US/09/543,681A CURRENT FILING DATE: 2000-04-05 PRIOR FILLNG DATE: 2000-04-05 PRIOR APPLICATION NUMBER: US 60/128,706 PRIOR FILING DATE: 1999-04-09 NUMBER OF SEQ ID NOS: 8344 SEQ ID NO 7770 Query Match Best Local S Matches 7 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid TITLE OF INVENTION: Thereby FILE REFERENCE: 2750-0876p CURRENT APPLICATION NUMBER: US/09/573,655A CURRENT FILING DATE: 2000-05-18 NUMBER OF SEQ ID NOS: 3280 SOFTWARE: Patentin version 3.0 SOFTWARE: Patentin version 3.0 LENGTH: 88 TYPE: PRT :| | |||| 290 SFSGVIATDT 299 Local Similarity 70.0 Local Similarity 70.0 1 TFIGAIATDT 10 71.4%; Score 35; DB Pred. No. 12; 1; Mismatches 5, Length 419; Indels 0, Gaps 0

Query Match Best Local Similarity

69.4%;

Score Pred.

34; No.

DB 5; 3.5;

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, NAME/KEY: misc_feature
; LOCATION: (1)...(101)
; OTHER INFORMATION: Xaa ~ X or * as
PCT-US01-08631-45049
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                US-09-543-681A-6920
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                                                                                                                                                                                                                                                                               APPLICANT: Griffels, R.
APPLICANT: Griffels, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
- CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 45049, Application PC/TUS0108631 GENERAL INFORMATION:
Sequence 6920, Application US/09543681A
                                                                                                                                             Query Match 69.4
Best Local Similarity 88.9
Matches 8; Conservative
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SOFTWARE: CUSTOM
SEQ ID NO 45049
LENGTH: 101
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR EILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
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TYPE: PRT
                                                                                                                                                                                                                                        ORGANISM: Chlamydia pneumoniae
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                                                                               233 FIGAIATLT 241
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Best Local
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; SEQ ID NO 390
; LENCTH: 248
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-602-740-390
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US-09-738-626-5009
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US-09-602-740-390
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APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRA
TITLE OF INVENTION: DIGNOSTICS AND THERAPEUTICS
EILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                   Sequence 5009, Application US/09738626 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 390, Applic GENERAL INFORMATION:
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Best Local Similarity
Matches 6; Conserv
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY
TITLE OF INVENTION: PRODUCTION
FILE REFERENCE: BGI-126CP
CURRENT PRILICATION NUMBER: US/09/602,740
CURRENT FILING DATE: 2001-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 784
                                                                                                                                             APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Pompejus, Markus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Proteus mirabilis
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58 TSLGALAVDT 67
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Zelder, Oskar
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                 SENOH,
OZAKI,
                                                     YOKOI, HARUHIKO
TATEISHI, NAOKO
                                                                                     HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                              MIZOGUCHI, HIROSHI
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Pred. No. 18;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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27;
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 248
                                                                                                                                                                                                                                                                                                                                                                          Indels
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OF INVENTION: NOVEL POLYNUCLEOTIDES

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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER: OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN NOS: 7059
SOFTWARE: PATENTIN Ver. 3.0
SEQ ID NO 5009
RESULT 9
US-09-864-761-40366
; Sequence 40366, Application US/09864761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/209,467
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2300
LENGTH: 476
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2300, Application PC/TUS0118569
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
                                                                                                                                                                        Query Match
Best Local
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CURRENT FILING DATE: 2001-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA133PCT
                                                                                                                                                                                                                                                      NAME/KEY: SITE LOCATION: (474) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: SITE
LOCATION: (377)
                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE LOCATION: (470)
OTHER INFORMATION: Xaa equals
                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
LOCATION: (437)
OTHER INFORMATION:
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61 TMIGAVGTD 69
                                                                                        450
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les 6; Conserv
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                                                                                     TFLGALAVGT 459
                                                                                                                                                       Similarity
6; Conser
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                                                                                                                                                                    67.3%;
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                                                                                                                                                                    Score 33;
Pred. No.
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Pred. No.
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37;
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23;
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SOFTWARE: Annomax Seque.
SEQ ID NO 40366
LENGTH: 58
TYPE: PRT
                                                        Query Match
Best Local Similarity
Matches 6; Conser
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PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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PRIOR APPLICATION NUMBER: US 60/207,456
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PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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                                                                                                                                                                                                          OTHER INFORMATION: MAP TO AC008468.4

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.96

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.89

OTHER INFORMATION: EXPRESSED IN BDULT LIVER, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/US01/00662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Penn, Sharron G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
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  TFIGAIATD
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                                                           Conservative
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                                                                                65.3%;
66.7%;
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                                                        Score 32; DB
Pred. No. 5.9;
1; Mismatches
                                                                                   5.9;
                                                                                                           5;
                                                                                                         Length 58
                                                        0;
                                                     Gaps
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR PRILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 38445
LENGTH: 85
TYPE: no.
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Sequence 38445, Application US/09864761
OTHER INFORMATION: -09-864-761-38445
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21
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                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OR APPLICATION NUMBER: PCT/US01/00664
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00669
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00665
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00668
OR FILING DATE: 2001-01-30
OR FILING DATE: 2001-01-30
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INFORMATION:
INFORMATION:
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: EXPRESSED IN PLACE:
: EXPRESSED IN LUNG,
: EXPRESSED IN FETAL
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EXPRESSED
                                                      EXPRESSED SWISSPROT
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                       EST_HUMAN
                                                                                                             EXPRESSED
                                              ED IN PLACENTA, SIGNAL = 1.2

ED IN LUNG, SIGNAL = 1.5

ED IN FETAL LIVER, SIGNAL = 2.2

ED IN BRAIN, SIGNAL = 1.8

ED IN ADULT LIVER, SIGNAL = 1

ED IN HEART, SIGNAL = 1

ED IN HEART, SIGNAL = 3

ED IN HEART, SIGNAL = 3

ED IN BONE MARROW, SIGNAL = 1.2

FILTE : 095865, EVALUE 8.30+00
                            HIT: A1969295.1, EVALUE
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Query Match

65 .38;

Score 32; DΒ ŝ

Application US/09543681A

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NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 31598
LENGTH: 131
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-08631-31598
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RESULT 13
US-09-543-681A-8195
; Sequence 8195, App
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                                                                                                      8
                                                                                                                         Query Match
Best Local Similarity
""" hes 6; Conserv
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PCT-US01-08631-31598
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SOFTWARE: Custom
SEQ ID NO 31597
LENGTH: 131
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APPLICANT: Hyseq, Inc
TITLE OF INVENTION: N
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Best Local
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CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-03-31 PRIOR APPLICATION NUMBER: 09/PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: PCT/US01/08631 CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES FILE REFERENCE: 21272-049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
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es 6; Conserv
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                                                                             TFVGRIAQD
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                                                                                                                                       Score 32; DB Pred. No. 15; 1; Mismatches
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l; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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PCT-US01-08631-31599

Sequence 31599, Application PC/TUS0108631

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REFERENCE: 21272-049

CURRENT APPLICATION NUMBER: PCT/US01/08631

CURRENT FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: 09/540,217

PRIOR FILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: 09/649,167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : LENGTH: 460
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-8195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: GARY BRETON
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR PRILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 8195
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
CURRENT EPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR PILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 60181
LENGTH: 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1)...(475)
OTHER INFORMATION: Xaa - x or * as defined in Table 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1:|||||
361 FVGAIAT 367
                                                                                                                                                                                                                                                                                             111: 111
209 IGAVKTDT 216
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB Pred. No. 61;
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NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
SEQ ID NO 31599
                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (1)...(650)
OTHER INFORMATION: Xaa = X or * as defined in Table 2
                                                                                                                                                                                                              NAME/KEY: DOMAIN
LOCATION: (178)...(196)
OTHER INFORMATION: CADHERIN SIGNATURE domain identified by eMATRIX, accession
OTHER INFORMATION: number PR00205B, p-value=1.706e-11, raw score of 11.39
                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                    LENGTH: 650
||:| || |
21 TFVGRIAQD 29
                               1 TFIGALATD 9
                                                                Conservative
                                                                                 65.3%;
66.7%;
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                                                                               Score 32;
Pred. No.
                                                                 Mismatches
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                                                                 Gaps
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Search completed: September 28, 2001, 12:38:05 Job time: 773 sec

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Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
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seq length:
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112:
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Gapop 10.0 , Gapext 1.0
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30
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.

Score

Query Match Length DB

ID

Description

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16 25 28 18	16 16 16 17 16 16	117 128 127 127 127	220 220 220 230 24 24 24 24 25 26 26 27	22 49 52
-09-248 797-429 -09-833 790-440 -09-248-797-306 -09-644-871-691 -09-833-790-177 -09-474-436-251 -09-726-810-860	-649-164-6809 -287-618-1869 -287-618-1869 -234-611-7813 -235-076-1312 -248-797-3067 -332-782-1312 -737-223-1312 -234-611-5892		-09-705 -09-705 -09-534 -09-134 -09-070 -09-070 -60-045 -60-045 -09-371 -09-244 -09-281	S-09-551-645-2 -07-742-128-1 S-60-177-571-2486 T-US01-00663-1010 S-60-205-418-265
nce 4292 nce 440, nce 3067 nce 6919 nce 177, nce 2512 nce 860,	28, 28, 28, 28, 28, 28, 28, 28, 28, 28,	nce 488, Apnace 20613, ance 20613, proce 3245, proce 1815, proce 10305, ance 10305, ance 1042, proce 1042, proce 1042, proce 13740	e 21257 A e 1149, Ap e 1149, Ap e 3194, Ap e 3194, Ap e 202, Ap e 203, Ap e 11165, A e 117812, e 157812, e 117813, e 110532, e 110532, e 10258, e 10258,	2, Appl 1, Appli 2486, A 10104, A 265, Ap

ALIGNMENTS

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; FEATURE: ; OTHER INFORMATION: The epitope recognized by SRT10 US-09-551-645-2
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NAME: Spevack, A. David
REGISTRATION NUMBER: 24.743
REFERENCE/DOCKET NUMBER: N.C.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 295-6759
TELEPHONE: (301) 295-4033
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5319 base pairs
                                                                                                                                                                             CLASSIFICATION: 424

ATTORNEY/AGENTT.

**LODPY disk**

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/07/742,128

FILING DATE: 19910809

CLASSIFICATION: 424

ATTORNEY/AGENTT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/551,645
CURRENT FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 30
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09551645
GENERAL INFORMATION:
APPLICANT: HAIN, MYONG-JOON
TITLE OF INVENTION: NEW EPITOPE TAG RECOGNIZED BY A MONOCLONAL ANTIBODY TO
TITLE OF INVENTION: RICKETTSIA TYPHI
FILE REFERENCE: 105997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 30; DB 22; Length 30; Best Local Similarity 100.0%; Pred. No. 0.0059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Rickettsia typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Gene and Protein Applicable to the TITLE OF INVENTION: Preparation of Vaccines for and the Detection TITLE OF INVENTION: Rickettsia Typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Counsel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dobson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bethesda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Counsel, Naval Medical Res & Dev Cmd National Naval Medical Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ching, Wei Mei
Dasch, Gregory A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carl, Mitchell NMI
                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
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CURRENT APPLICATION NUMBER: US/60/177,571
CURRENT FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 5082
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2486
ELENGTH: 566
TYPE: DNA
ORGANISM: HUMAN
US-60-177-571-2486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 5319 US-07-742-128-1
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Best Local Similarity
Watches 29; Conserve
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                                                              Query Match
Best Local
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TITLE OF INVENTION: ISOLATED HUMAN S
TITLE OF INVENTION: NUCLEIC ACID MOL
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNI
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Ricke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBLICATION INFORMATION:
AUTHORS: Carl, M.
AUTHORS: Dobson, M. E.
AUTHORS: Dobson, M. E.
AUTHORS: Ching, W. -M.
AUTHORS: Dasch, G. A.
TITLE: Characterization of the gene encoding the
TITLE: protective S-layer protein of Rickettsia
TITLE: prowazekii; presence of a truncated identi
TITLE: homolog in rickettsia typhi
TITLE: homolog in rickettsia typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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NAME/KEY:
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LOCATION:
                                              Local Similarity 80.0 nes 24; Conservative
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1 acatttataggagctattgctacagataca 30
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379..386
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363..368
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391..5226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.78;
                                                              68.0%;
                                                           Score 20.4; DB 45
Pred. No. 1.6e+02;
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                                              Mismatches
                                                                             DB 49;
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                                                                                                                                                                                                                                                                                                 HUMAN SECRETED PROTEINS,
                                                                              566;
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                                                Gaps
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238 acattaattagaaccattgttacagataca 267

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CURRENT APPLICATION NUMBER: PCT/USO1/0063

CURRENT FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/180, 312

PRIOR FILING DATE: 04 February 2000 (04.02.00)

PRIOR APPLICATION NUMBER: US 60/207, 456

PRIOR APPLICATION NUMBER: US 60/207, 456

PRIOR APPLICATION NUMBER: US 99/632,366

PRIOR PILING DATE: 03 August 2000 (03.08.00)

PRIOR FILING DATE: 03 October 2000 (03.10.00)

PRIOR PRIOR APPLICATION NUMBER: US 60/236,356

PRIOR FILING DATE: 07 September 2000 (27.09.00)

PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR FILING DATE: 27 September 2000 (21.09.00)

PRIOR FILING DATE: 21 September 2000 (21.09.00)

PRIOR PRIOR PRIOR PRIOR APPLICATION NUMBER: US 60/234,887

PRIOR APPLICATION NUMBER: US 90/608,408

PRIOR FILING DATE: 31 June 2000 (30.06.00)

PRIOR FILING DATE: 30 June 2000 (30.06.00)

PRIOR FILING DATE: 30 June 2000 (30.06.00)

PRIOR FILING DATE: 30 June 2000 (30.06.00)
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; Sequence 265, Application US/60205418
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: MAP TO AC025119.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL -
PCT-US01-00663-10104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US01-00663-10104
                                                                               LENGTH: 6063
TYPE: DNA
ORGANISM: HUMAN
S-60-205-418-265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Molecular Dynamics Sequence Listing Engine SEQ ID NO 10104
LENGTH: 600
                                                                                                                                                                                            SEQ ID NO 265
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Best Local Similarity
                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/60/205,418
CURRENT FILING DATE: 2000-05-19
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Beasley, Ellen TITLE OF INVENTION: ISOLATITLE OF INVENTION: NUCLEI TITLE OF INVENTION: USES
                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Penn, Sharion G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA
FILE REFERENCE: PB 0004 MO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
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68.0%;
                                                                                                                                                                                                                      Windows Version 4.0
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Pred. No. 1.6e+02
); Mismatches
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Query Match

Score 20.4;

В 52;

Length 6063;

APPLICANT: APPLICANT:

Last, Robert Levin, Irena M. Norris, Susan R

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FILE REFERENCE:

38-10(15478)B
CURRENT APPLICATION NUMBER: US/09/505,532
CURRENT FILING DATE: 2000-02-16
PRIOR FILING DATE: USSN 60/120,645 1999
PRIOR PRIOR OF SEQ ID NOS: 51470
SEQ ID NO 11257
LENGTH: 580
TYPE: DNA
ORGANISM: Arabidopsis thaliana columbia
US-09-505-532-11257
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                                        US-09-534-859-149
                                                      RESULT
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; ORGANISM: Lycopersicon esculentum
US-09-705-926-2517
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; GENERAL INFORMATION: Bu
                          Sequence 149, Application US/09534859
                                                                                                                                                                  Query Match
Best Local
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LENGTH: 1217
                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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CURRENT EILING DATE: 2000-11-06
NUMBER OF SEQ ID NOS: 21624
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Best Local :
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                                                                                                                                                                                                                                                                                                                                            APPLICANT: Liu, Jingdong APPLICANT: Wiegand, Roge TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Timberlake, William E.
TITLE OF INVENTION: Plant Ge
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                            2 catttataggagctattgctacagatac 29
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                                                                                                                                                    l Similarity
23; Conserv
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23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09705926
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Bush, David F
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82.1%;
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82.1%;
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ussn 60/120,645 1999-02-18; ussn 09/443,025 1999-11-12;
51470
                                                                                                                                                                                                                                                                                                                                                 ANNOTATED PLANT GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Genome Sequences and Uses Thereof
                                                                                                                                                   Score 20; DB Pred. No. 2.7e 0; Mismatches
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Pred. No. 2.3e
0; Mismatches
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5;
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2.7e+02;
hes 5;
                                                                                                                                                                               Length 1217;
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CURRENT APPLICATION NUMBER: US/09/534,859; CURRENT FILING DATE: US/09/534,859; NUMBER OF SEQ ID NOS: 1127; SEQ ID NO 149; LENGTH: 89138; TYPE: DNA ORGANISM: Arabidopsis thaliana US-09-534-859-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-60-068-175-649/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 649, Application US/60068175 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                    APPLICATION NUMBER: US/60/068,175
FILING DATE: HEREWITH
CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 9132
REFERENCE/DOCKET NUMBER: PM-0009-2 P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1055-01555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                         TELEFAX: (650) 845-416 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24610 cctttataggagcgattgcttcagctgc 24637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Finney, Gregory L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF STREPTOCOCCUS PNEUMONIAE
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 1175
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 434 base pairs
         IMMEDIATE SOURCE
                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                 TOPOLOGY:
                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: PALO ALTO
STATE: CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 94304
                                                                                 nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parnell, Laurence D.
SPN2c651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: INCYTE PHARMACEUTICALS, INC 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corley, Neil C.
Russo, Frank D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heath, Joe D
                                                 circular
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                                 genomic DNA
                                                                    double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roger C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steven D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLANT POLYMORPHIC MARKERS AND USES THEREOF
                                                                                                                                          649:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Pred. No. 5.9e+02;
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Query Match

65.3%;

Score 19.6;

DB 38;

Length 434;

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US-09-134-000-3194/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 6810
SEQ ID NO 3194
LENGTH: 930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                         COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 98369
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS TITLE OF INVENTION: FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-005
CURRENT APPLICATION NUMBER: US/09/134,000A
CURRENT FILING DATE: 1998-08-13
              TELEFAX: (3
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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|| ||||| |||| ||||| ||||| |||||
381 ATGTATAGTAGCTTTTGCTAGAGATA 356
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                                                                                                                                                                                                                                                                                                                                                                                                STATE: Maryland
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                                                                                                                                                                                                                                                                                                                                                                                                              T: 9410 Key West Avenue
Rockville
                                                                                                                                                                                                                                                                                                                                                                 20850
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CHARACTERISTICS:
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              (301) 309-8512
OR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                USA
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Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                         E: Diskette, 3.50 inch, 1.4Mb storage HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Genome Sciences,
                                                                                                                                                                                                                                                                                             MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterococcus faecialis Polynucleotides and Polypeptides
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0; Mismatches
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Pred. No. 3.
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                                                                                                      Query Match
                                                                     Matches
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                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
 9681
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                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION UNBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 10996 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                    Local Similarity
nes 22; Conser
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les 22; Conserv
                    3 atttataggagctattgctacagata 28
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                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ATGTATAGTAGCTTTTGCTAGAGATA 9656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                        STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                  TELEFAX: (301)
                                                                                                                                                                                                                                                                                                                                                    NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                   TELEPHONE: (301) 309-8504
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                                                                                65.3%;
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                                                                                    Score 19.6;
Pred. No. 6
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Pred. No. 6
                                                                    Mismatches
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                                                                                  6; DB 14;
6e+02;
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                                                                                                   Length 10996;
                                                                    Indels
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US-60-045-649-1115/c
                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                     Sequence 1106, Application US/60046653 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                           8280 ATGTATAGTAGCTTTTGCTAGAGATA 8255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                              CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hann, Amy L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF ENTEROCOCCUS FAECALIS
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 1466
                                                              TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF ENTEROCOCCUS FAECALIS TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF NUMBER OF SEQUENCES: 1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION UNMBER: 39,132
REFERENCE/DOCKET NUMBER: PM-0003P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
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CLONE: EF1c1115
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/60/045,649
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Russo, Frank D.
Hann, Amy L.
Heath, Joe D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (415) 855-0555
(415) 845-4166
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Russo, Frank D.
                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                 Lagace, Robert E.
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Pred. No. 7
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COUNTRY:

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; IMMEDIATE SOURCE:
; CLONE: EFA1C1106
US-60-046-653-1106
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NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PM-0003-1 P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 85-0555
TELEFAX: (415) 85-0555
INFORMATION FOR SEQ ID NO: 1106:
SEQUENCE CHARACTERISTICS:
LENGTH: 31984 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-60-068-217-974/c
             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/60/068,217

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

ARAME: CERRONE, MICHAEL C.

REGISTRATION NUMBER: 39,132

REFERENCE/DOCKET NUMBER: PM-0003-5 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 974, Application US/60068217 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1239

CORRESPONDENCE ADDRESS:
ADDRESSE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8280 ATGTATAGTAGCTTTTGCTAGAGATA 8255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hann, Amy L.
APPLICANT: Heath, Joe D.
APPLICANT: Finney, Greedry L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF ENTEROCOCCUS FAECALIS
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Corley, Neil C. APPLICANT: Russo, Frank D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: HEREWI CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                 COUNTRY:
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84.6%; Pred. No. 7.3e+02
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; TOPOLOGY: circula
; MOLECULE TYPE: geno
; IMMEDIATE SOURCE:
; CLONE: EFALC974
US-60-068-217-974
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                                                                                                                                                                                                                     TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 974:
SEQUENCE CHARACTERISTICS:
LENGTH: 32081 base pairs
TYPE: nucleic acid
                                                          Query Match 65.3%; Score 19.6; Best Local Similarity 84.6%; Pred. No. 7. Matches 22; Conservative 0; Mismatche
STRANDEDNESS:
                                                                                                                                                                                              circular
                                                                                                                                                                                genomic DNA
                                                                                                                                                                                                             double
                                                                                                                                                                                                                                                                        974:
                                                               Mismatches
                                                                                .3e+02
                                                                                            DB 38;
                                                                                           Length 32081;
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Gaps

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Search completed: September 28, 2001, 10:56:19 Job time: 3364 sec

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Maximum Match 100%
Listing first 45 summaries
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2: /cgnl_7/ptodata/2/pna/U

3: /cgnl_7/ptodata/2/pna/U

4: /cgnl_7/ptodata/2/pna/U

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6: /cgnl_7/ptodata/2/pna/U

6: /cgnl_7/ptodata/2/pna/U

8: /cgnl_7/ptodata/2/pna/U
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Match
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[17/ptodata/2/pna/US06_NEW_COMB.seq:*
[17/ptodata/2/pna/US07_NEW_COMB.seq:*
[17/ptodata/2/pna/US08_NEW_COMB.seq:*
[17/ptodata/2/pna/US09_NEW_COMB.seq:*
[17/ptodata/2/pna/US09_NEW_COMB.seq1:*
[17/ptodata/2/pna/US09_NEW_COMB.seq2:*
[17/ptodata/2/pna/US09_NEW_COMB.seq2:*
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US-09-864-761-12782
US-09-803-736-149
US-60-253-652-7674
US-08-798-074B-10268
US-08-798-074C-10268
US-08-798-074C-10268
US-08-798-074C-10268
US-08-798-074C-10268
US-09-904-809-7813
US-09-904-809-892
US-09-652-125A-8012
PCT-USO1-08631-16714
US-09-818-601-3927
US-09-818-601-3927
US-09-818-601-3927
US-09-808-601-3927
US-09-808-601-3927
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US-09-808-601-3927
US-09-808-764-905-36889
US-09-764-905-36889
US-09-803-736-234
US-09-803-736-234
US-09-913-154-748
US-09-317-311C-234
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Sequence 12782, A
Sequence 7674, App
Sequence 10268, A
Sequence 10268, A
Sequence 10268, A
Sequence 10268, A
Sequence 12293, A
Sequence 5892, Ap
Sequence 6801, Ap
Sequence 16714, Ap
Sequence 3525, Ap
Sequence 3525, Ap
Sequence 3527, Ap
Sequence 3527, Ap
Sequence 3724, App
Sequence 2714, Ap
Sequence 2714, Ap
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Sequence 2714, App
Sequence 274, App
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61.3	61.3	62.0	62.0	62.0	62.0	62.0	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	
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sequence 12300, A		Sequence 1467, Ap	Sequence 1467, Ap	Sequence 15517, A	Sequence 10317, A	Sequence 13288, A	Sequence 1145, Ap	Sequence 1216, Ap	Sequence 1632, Ap	Sequence 5569, Ap	Sequence 1631, Ap	Sequence 4648, Ap	Sequence 9459, Ap	Sequence 82, Appl	Sequence 24, Appl		Sequence 8557, Ap		Sequence 5112, Ap	

## ALIGNMENTS

Application US/09864761

7

PRIOR APPLICATION NUMBER: US 60/180, 312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PRILING DATE: 2000-09-21 US-09-864-761-12782
, Sequence 12782, Application (
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R. CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Aeomica-X-1 APPLICANT: Hanzel, David | APPLICANT: Chen, Wensheng APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30 David K. ACID PROBES USEFUL

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US-60-253-652-7674/c
; Sequence 7674, Application US/60253652
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: MAP TO AC025119.2
; OTHER INFORMATION: EXPRESSED IN BORIN SIGNAL = 0.45
; OTHER INFORMATION: EXPRESSED IN BOLL MARROW, SIGNAL = 0.54
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.56
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.52
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
US-09-864-761-12782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-803-736-149
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NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 12782
LENGTH: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 1582
SEQ ID NO 149
LENGTH: 89138
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bush, David F.
APPLICANT: Levin, Irena M.
APPLICANT: Norris, Susan R.
APPLICANT: Wiegand, Steven D.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
FILE REFERENCE: 38-10(1543))D
CURRENT APPLICATION NUMBER: US/09/803,736
CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 09/534,859
PRIOR APPLICATION NUMBER: 1dentifled by Attorney Docket number 04983.0206CPUS01 38-10
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
APPLICANT: Glenn, Matthew
APPLICANT: Grigor, Murray R
APPLICANT: Grigor, Murray R
TITLE OF INVENTION: Compositions isolated from bovine
TITLE OF INVENTION: tissues and methods for their use
FILE REFERENCE: 1055P2
CURRENT APPLICATION NUMBER: US/60/253,652
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 29954
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361
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82.1%;
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Pred. No. 50;
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Pred. No. 14;
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NAME/KEY: misc_feature; LOCATION: (264); OTHER INFORMATION: n equiv-
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NAME/KEY: misc_feature

LOCATION: (1)...(630)

OTHER INFORMATION: n =

US-60-253-652-7674
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US-08-798-074B-10268/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/011,617
PRIOR FILING DATE: 1996-02-13
NUMBER OF SEQ ID NOS: 13449
SEQ ID NO 10266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10268, Appl GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 7674
LENGTH: 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences,
FILE REFERENCE: PO-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/08/798,074B
CURRENT FILING DATE: 1997-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rosen, Craig A. APPLICANT: Dillon, Patric
                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
LOCATION: (118)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (220)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (206)
OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                          OTHER INFORMATION: n equals
                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: (235)
                                                                                                                                                                                                                                    OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                    NAME/KEY: misc_feature LOCATION: (226)
                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Bovine
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23; Conserv
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                                                         Conservative
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                                                                                                                                             equals a,t,g, or
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81.5%;
                                                                       64.78;
79.38;
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                                                                       Score 19.4;
Pred. No. 33;
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pred. No. 32;
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                                                                                      Length 268;
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US-08-798-074B-10268/c ; Sequence 10268, Application US/08798074B

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APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: Human Genes, Sequences, an

FILE REFERENCE: PO-22

CURRENT APPLICATION NUMBER: US/08/798,074C

CURRENT FILING DATE: 1997-02-12

PRIOR APPLICATION NUMBER: 60/011,617

PRIOR PILING DATE: 1996-02-13

NUMBER OF SEQ ID NOS: 13449

SEQ ID NO 10268

LENGTH: 268
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Best Local Similarity
Matches 23; Conserv
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CURRENT FILING DATE: 1997-02-12
PRIOR APPLICATION NUMBER: 60/011,617
PRIOR FILING DATE: 1996-02-13
NUMBER OF SEQ ID NOS: 13449
SEQ ID NO 10268
LENGTH: 268
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TITLE OF INVENTION: Human Genes, Sequences, and Expression Products
FILE REFERENCE: PO-22
                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen, Craig A. APPLICANT: Dillon, Patric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen, Craig A.
                                                  FEATURE: misc_feature
NAME/KEY: misc_feature
LOCATION: (118)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (235)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (206)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (118)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                               TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: (264)
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                    NAME/KEY: misc_feature LOCATION: (206)
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LOCATION: (226)
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THER INFORMATION: n equals a,t,g,
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Li, Haodong
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79.38;
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Pred. No. 33;
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Sequence 7813, Application US/09904809
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OB:
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; TITLE OF INVENTION NUMBER: US/09/904,809
; CURRENT APPLICATION NUMBER: US/09/904,809
; CURRENT ETLING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/234,611
; PRIOR FILING DATE: 1999-01-22
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                                                                                                                                                                                                                                                                                                      US-09-904-809-7813/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/60/253,378
CURRENT FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 40367
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12293
LENGTH: 395
TYPE: DNA
                                                                                            NUMBER OF SEO ID NOS: 21025
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12293, Application US, GENERAL INFORMATION:
APPLICANT: Havukkala, Ilkka J
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local :
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (226)
LOCATION: (226)
OTHER INFORMATION: n equals
NAME/KEY: misc_feature
LOCATION: (235)
                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (235)
OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (220)
OTHER INFORMATION: n equals
NAME/KEY: misc_feature LOCATION: (1)...(467)
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LOCATION: (264)
                                    FEATURE:
                                                                                 LENGTH: 467
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LOCATION: (226)
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wes 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 79...
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79.3%;
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Pred. No. 36;
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Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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Query Match

DB

Length 500;

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APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 2041-757
CURRENT APPLICATION NUMBER: US/09/904,809
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 09/234,611
PRIOR APPLICATION NUMBER: 09/234,611
PRIOR FILING DATE: 1999-01-22
NUMBER OF SEQ ID NOS: 21025
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5892
LENGTH: 480
                                                                                                                                                                                                                                                                                                                            US-09-652-125A-2073/c; Sequence 2073, Application US/09652125A
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Thes 23; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_feature
; LCCATION: (1)...(480)
; OTHER INFORMATION: n = A,T,C or
US-09-904-809-5892
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Best Local Similarity 79.3
Matches 23; Conservative
                                                                                                CURRENT APPLICATION NUMBER: US/09/652,125A CURRENT FILING DATE: 2001-08-30 PRIOR APPLICATION NUMBER: 60/151,127 PRIOR FILING DATE: 1999-08-30 NUMBER OF SEO ID NOS: 9506 SOFTWARE: FBStSEQ for Windows Version 4.0 SEQ ID NO 2073 LENGTH: 500
                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
APPLICANT: DiStefano, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5892, Appli GENERAL INFORMATION:
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                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES TITLE OF INVENTION: THEREFOR FILE REFERENCE: 1600.1189-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(500)
OTHER INFORMATION: n =
                                                                  ORGANISM: Homo sapiens
                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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79.3%;
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     A,T,C
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Pred. No. 37;
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Pred. No. 37;
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RESULT 12
PCT-US01-08631-16714/c
Sequence 16714, Application PC/TUS0108631
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US-09-652-125A-8012/c
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                                                                                    PCT-US01-08631-16714
Query Match
Best Local S
Matches 23
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APPLICANT: HYSEG, Inc.
APPLICANT: HYSEG, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
FILE REFERENCE: 21272-049
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/151,127
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 9506
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 8012
                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 16714
LENGTH: 2253
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Best Local :
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APPLICANT: DiStefano, Peter
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
TITLE REFERENCE: 1600.1189-001
CURRENT APPLICATION NUMBER: US/09/652,125A
CURRENT FILING DATE: 2001-08-30
                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 77
TYPE: DNA
                                                                                                   NAME/KEY: SIMILAR LOCATION: (57)..(800) LOCATION: (57)..(800) COTHER INFORMATION: 82% homologous to Homo sapiens nucleolysin TIAR, accession OTHER INFORMATION: number M96954, Smith-Waterman Score-1084.
                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 CATTCATAGCAGCTAATGCTGCAGCTGCA 231
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nes 23; Conserv
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 Similarity 23; Conserv
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79.38;
                   64.7%;
79.3%;
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                 Score 19.4;
Pred. No. 49;
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Pred. No. 37;
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                                   Length 2253;
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2 catttataggagctattgctacagataca 30

Conservative

Mismatches

6,

Gaps

US-09-838-601-3927/c

Application US/09838601

В

258 CATTCATAGCAGCTAATGCTGCAGCTGCA 230

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; NAME/KEY: misc_feature; LCCATION: (1)...(4873)
OTHER INFORMATION: n = A,T,C or
US-09-838-601-3927
                                                                                     ; FEATURE:
; OTHER INFORMATION: Genbank Accession No. W46404
US-09-880-107-3525
                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 3555
      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Best Local
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SEQ ID NO 3927
LENCTH: 4873
TYPE: DNA
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APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Dougle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -09-880-107-3525/c
Sequence 3525, Application US/09880107
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CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 60/100,944
                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR EILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: US 60/107,225
PRIOR EILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: US 60/126,902
PRIOR APPLICATION NUMBER: US 60/126,902
PRIOR APPLICATION NUMBER: US 09/397,761
PRIOR EILING DATE: 1999-09-17
PRIOR EILING DATE: 1999-09-17
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/211,379 PRIOR FILING DATE: 2000-06-14
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A TITLE OF INVENTION: MIDTERM PLACENTA LIBRARY FILE REFERENCE: 1600.1042-002
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Josep
APPLICANT: Scherf, Uwe
                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 4410
                                                                                                                                             ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 CATTCATAGCAGCTAATGCTGCAGCTGCA 415
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      63.3%;
81.5%;
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79.38;
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      Score 19;
Pred. No.
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Pred. No. 56;
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                         Length 445;
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Search completed: September 28, 2001, 12:25:03 Job time: 7286 sec

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                                                                                                                                         ; LOCATION: (1)...(461)
; OTHER INFORMATION: n = A,T,C or G
US-09-904-703-6861
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                                                                                                                                                                                                                                                       SEQ ID NO 6861
LENGTH: 461
                                                               Matches
                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                    APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: WOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-758CCN1
CURRENT APPLICATION NUMBER: US/09/904,703
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 09/210,298
PRIOR FILING DATE: 1998-12-09
NUMBER OF SEQ ID NOS: 17812
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                 NAME/KEY: misc_feature
                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 TTTTTAGAAGCTATTGGGACAGATTCA 338
49 TTGATAGCCGCTTTTGCTACAGATAGA 23
              4 tttataggagctattgctacagataca 30
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                                                               Conservative
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Pred. No.
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